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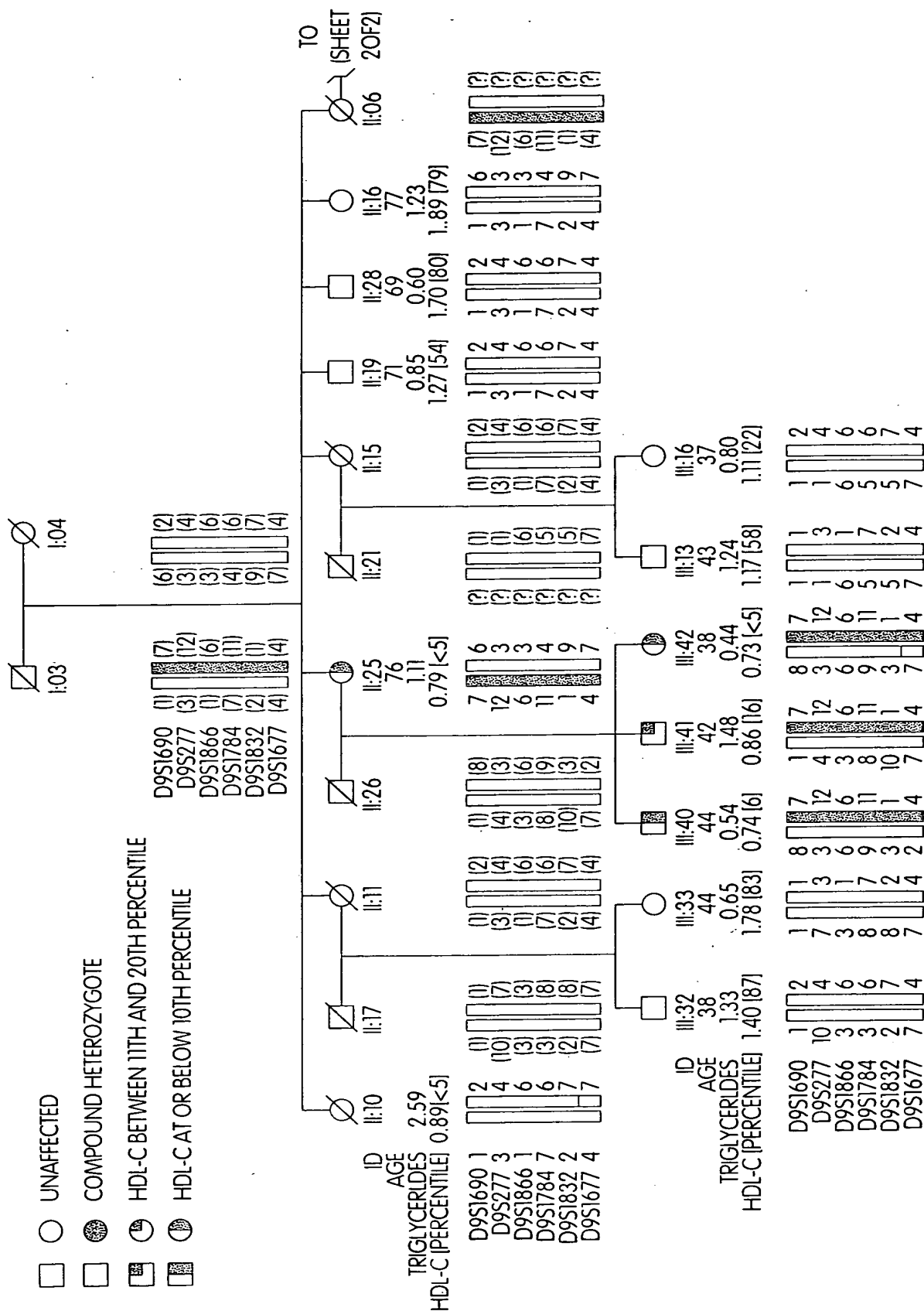


Fig. 1 (SHEET 1 OF 2)



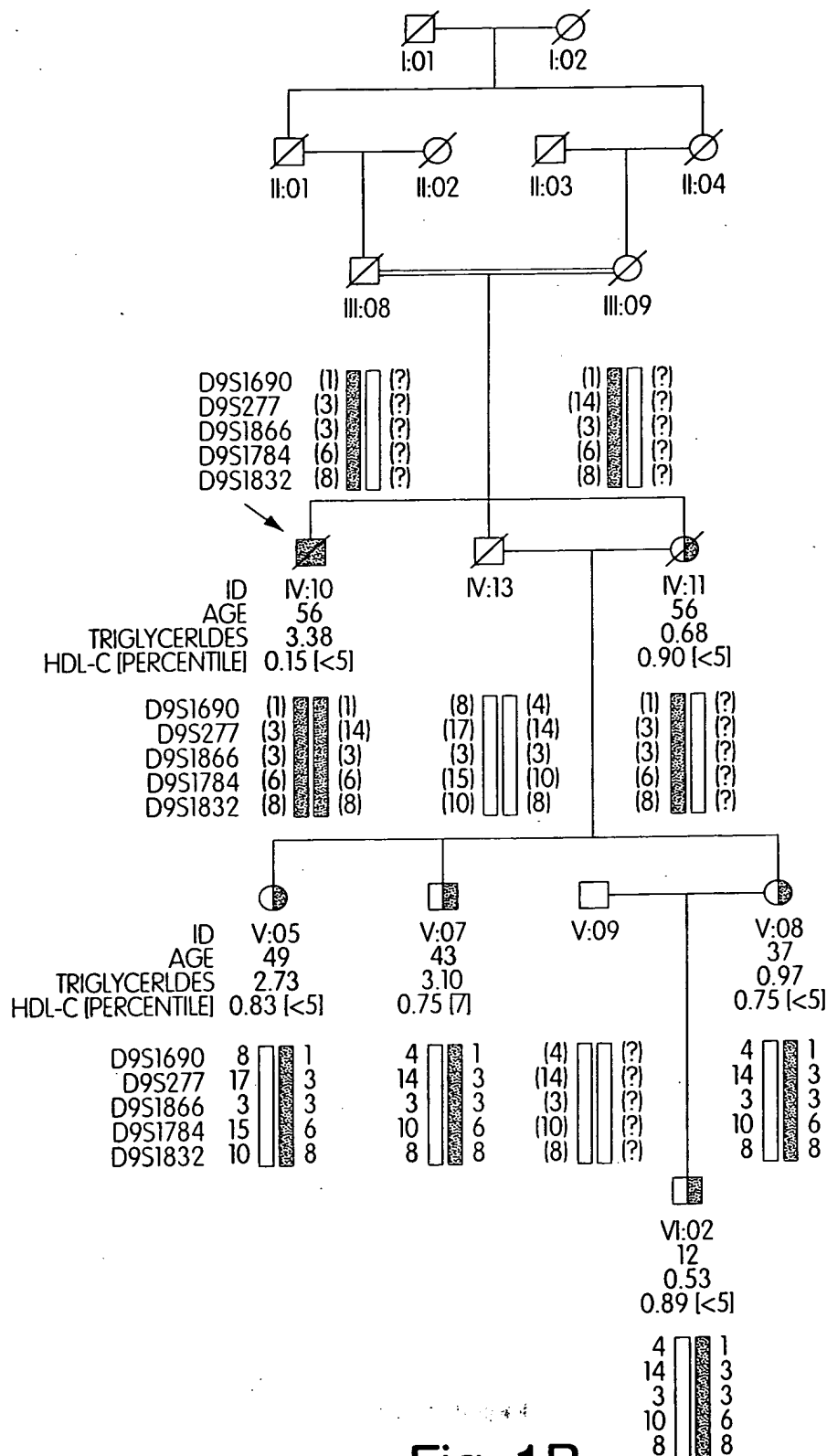


Fig. 1B

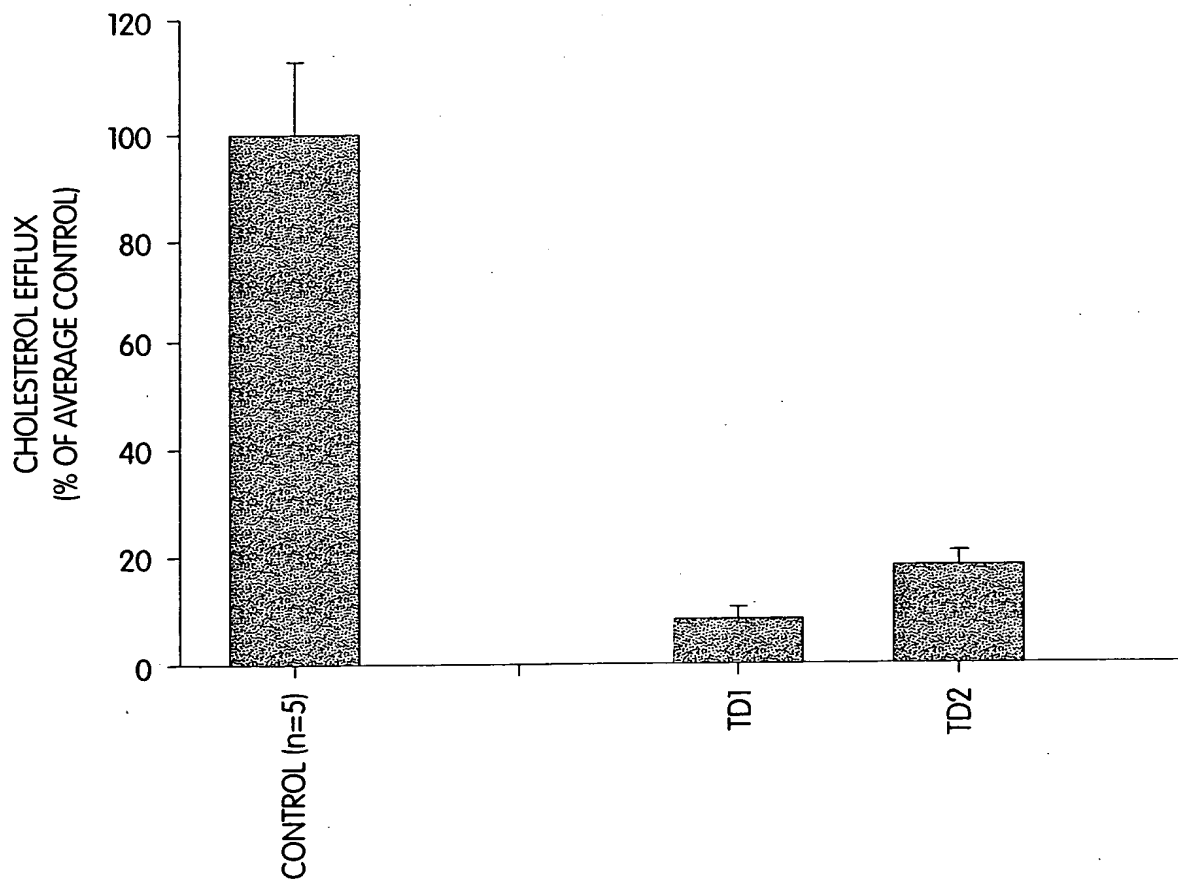


Fig. 1C



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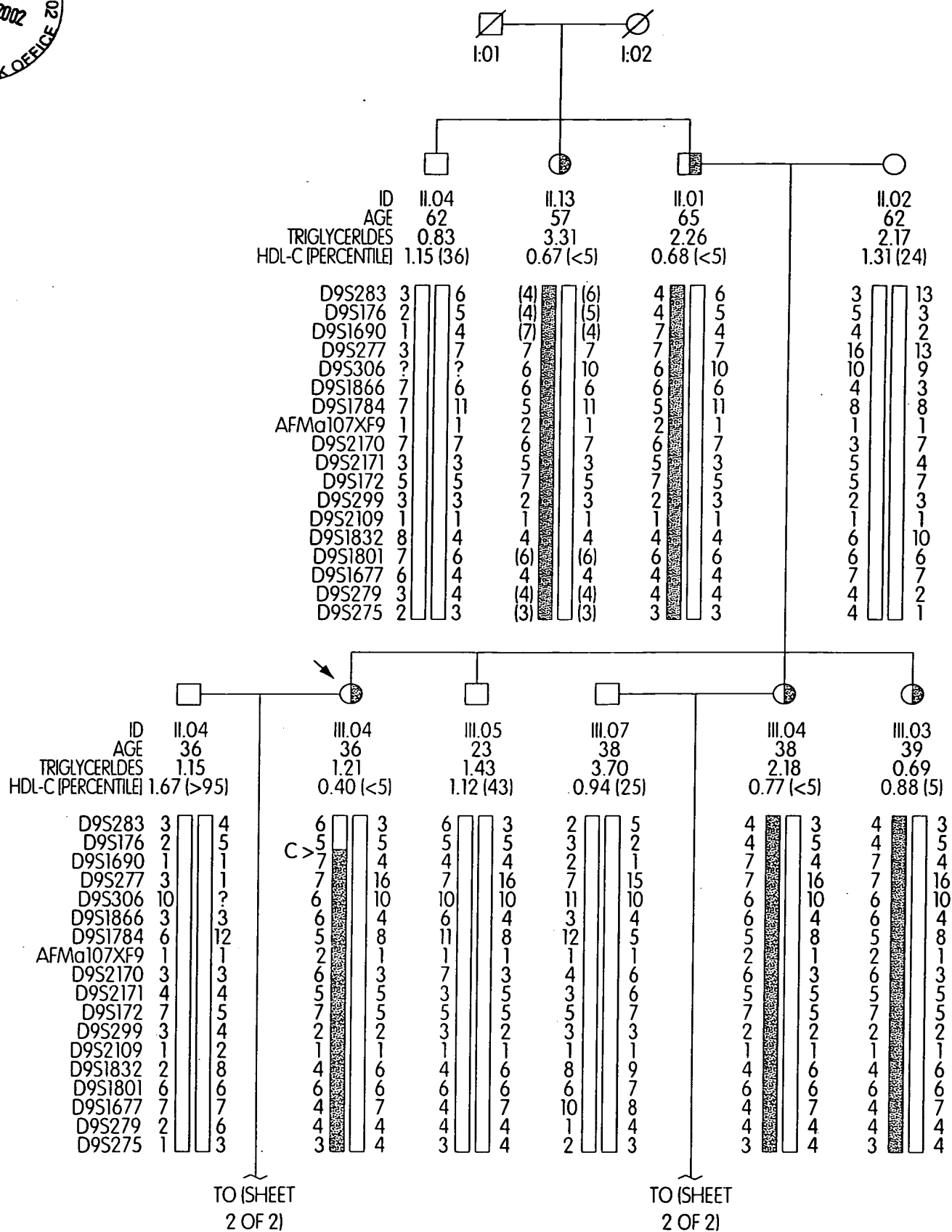


Fig. 2A (SHEET 1 OF 2)

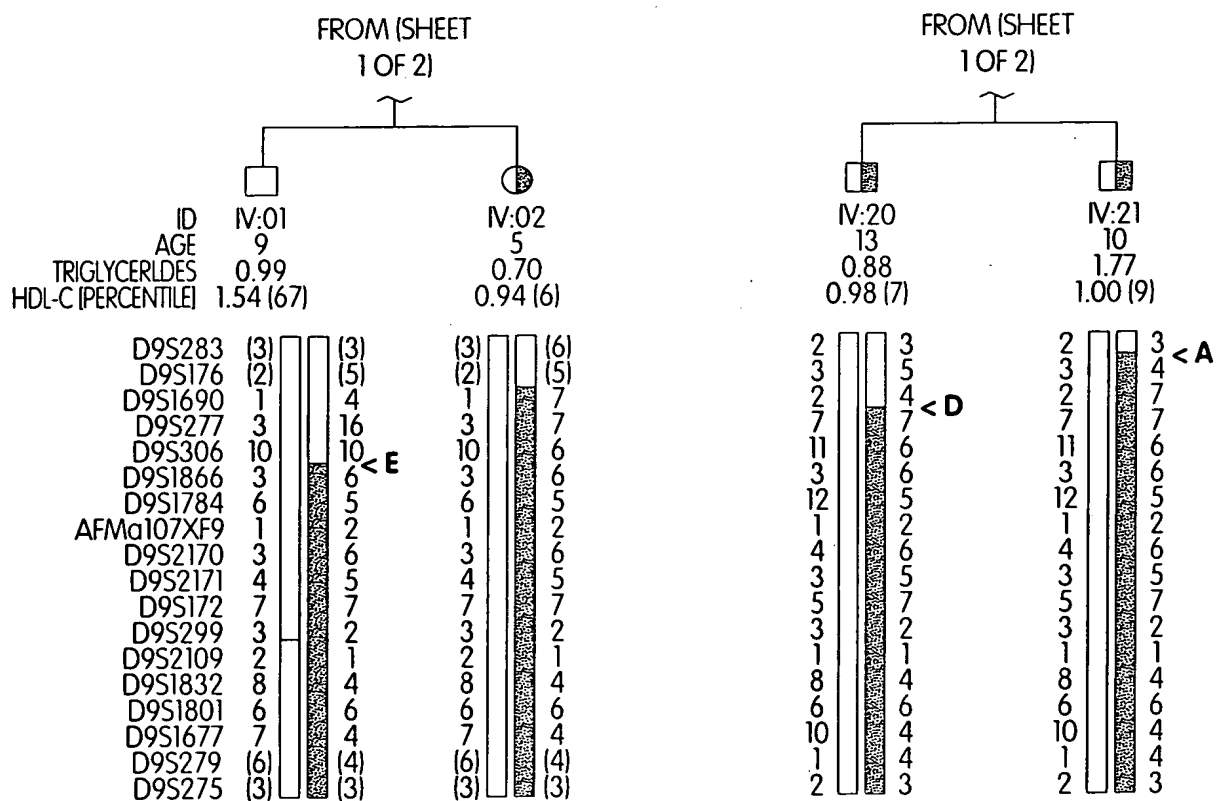
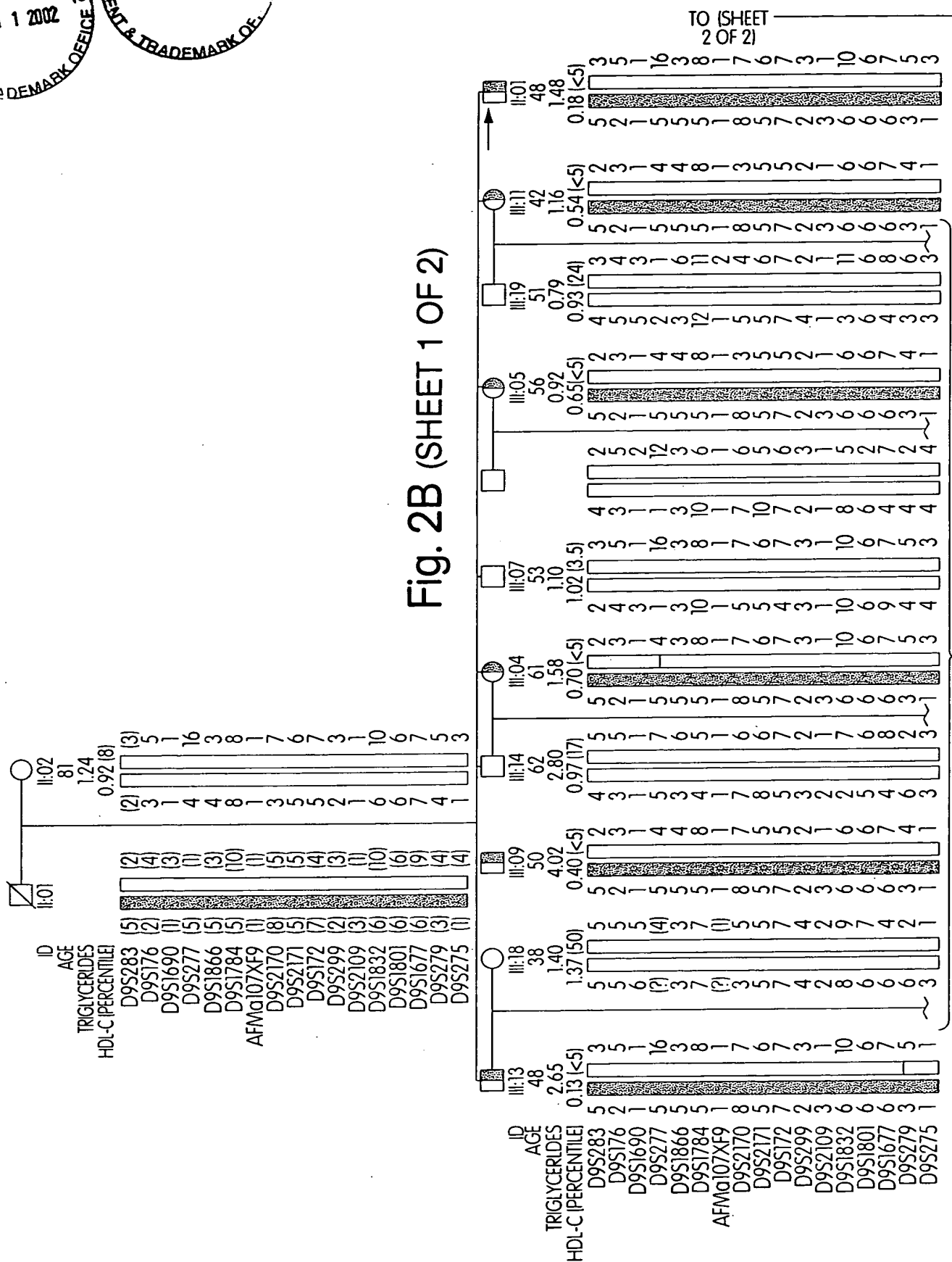


Fig. 2A (SHEET 2 OF 2)



Fig. 2B (SHEET 1 OF 2)





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FROM
SHEET
1 OF 2

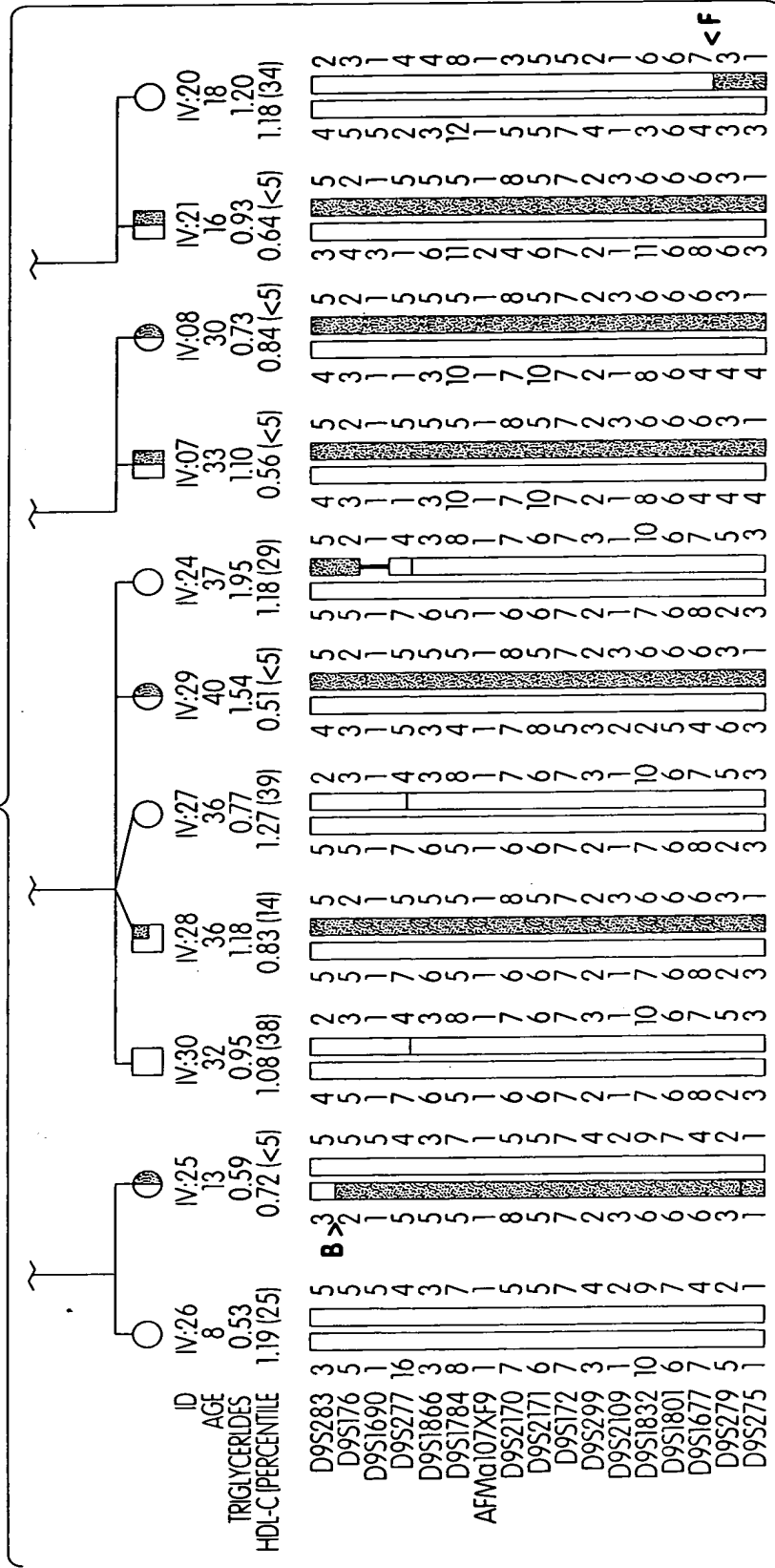


Fig. 2B (SHEET 2 OF 2)



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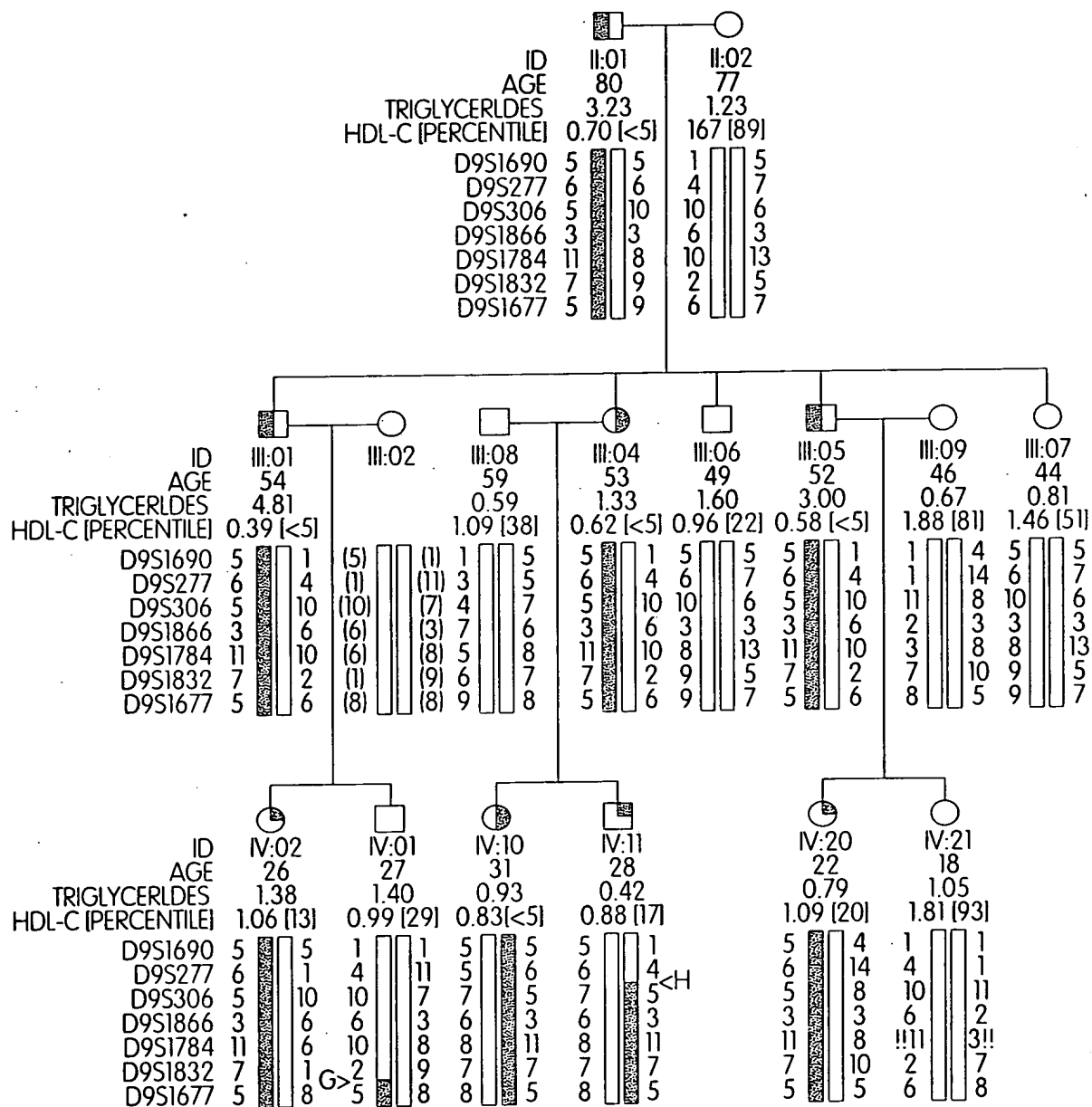


Fig. 2C



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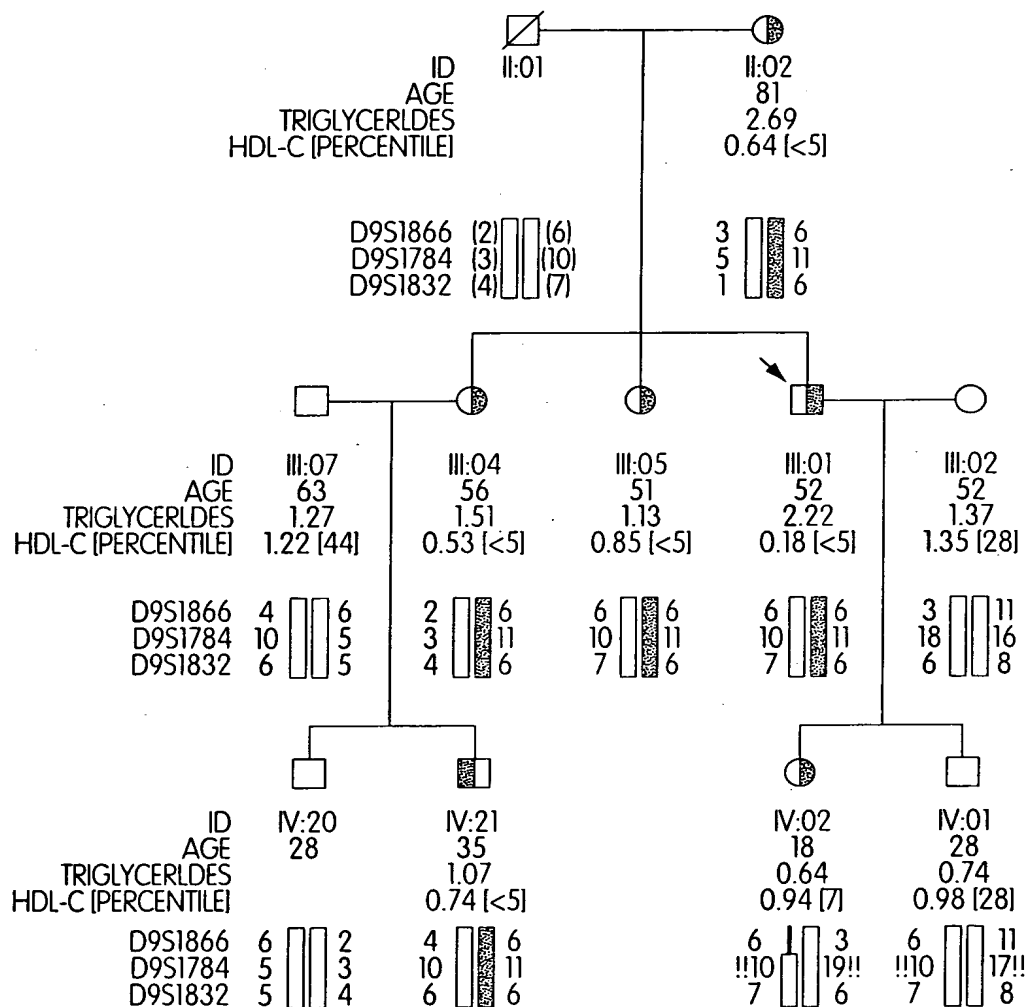
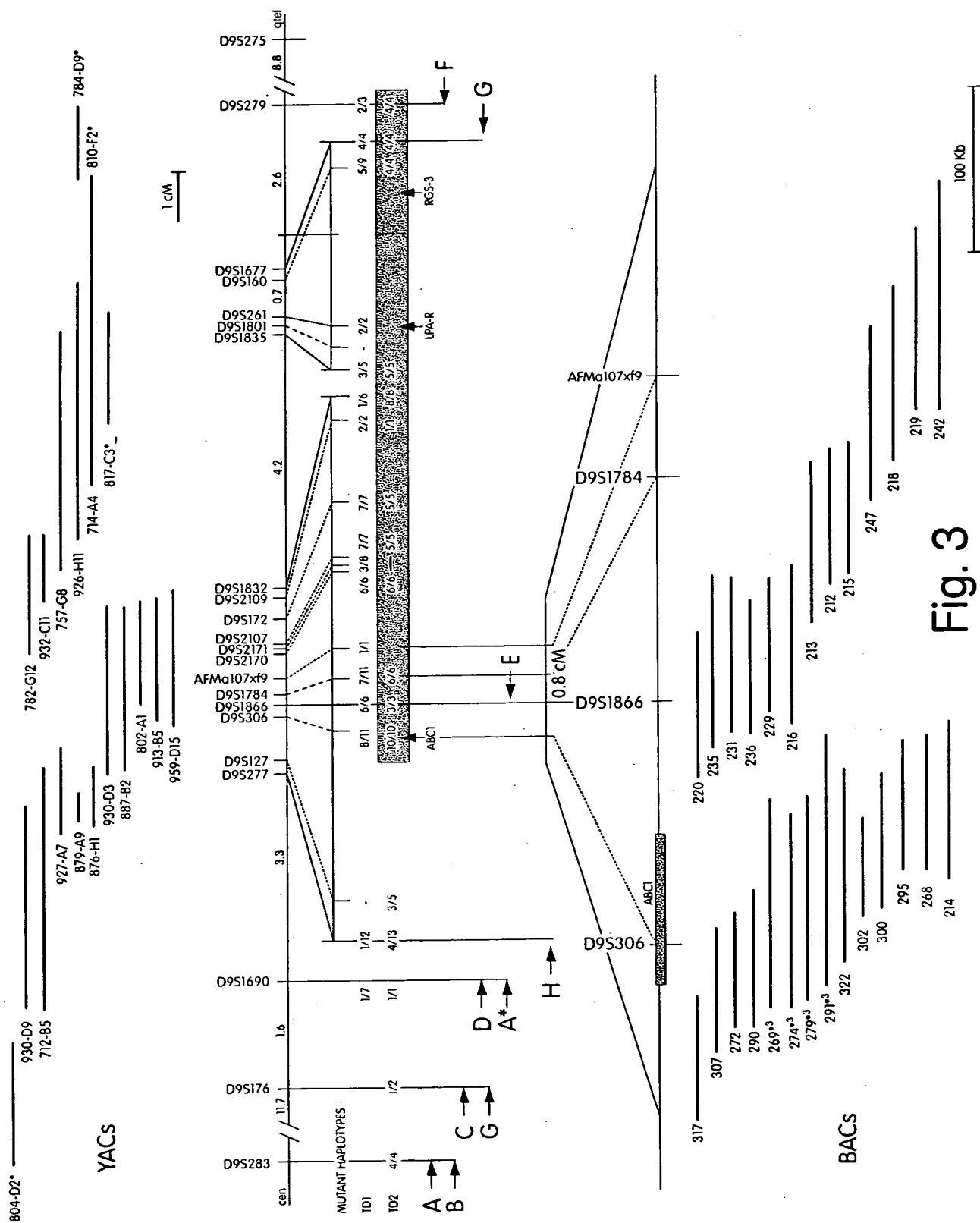
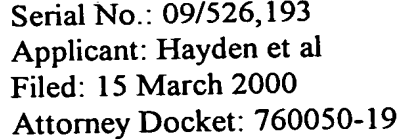


Fig. 2D

11

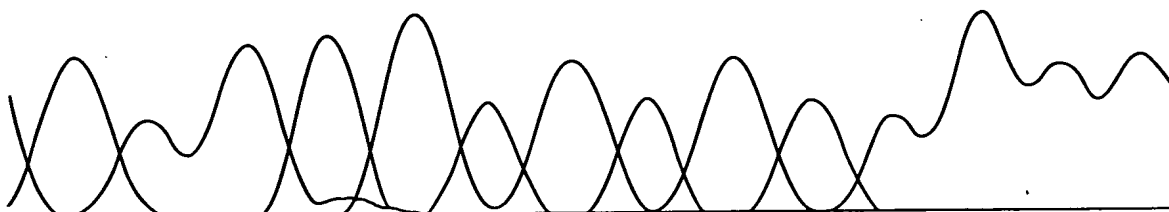




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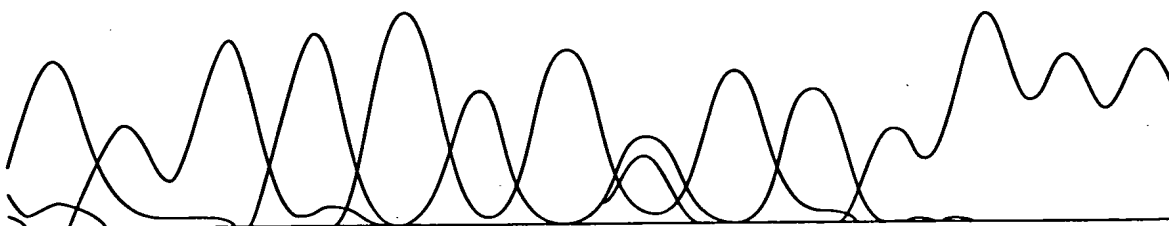
CONTROL

G C C T G T G T G T C C C C



FAMILY TD - 1, PATIENT III:01

G C C T G T G N G T C C C C



4496

T4503C (Cys1477Arg)

4509

Fig. 4A



Serial No.: 09/526,193
Applicant: Hayden et al
Filed: 15 March 2000
Attorney Docket: 760050-19

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EXON 20
TD-1

wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient

4485 4503 4529

a	a	a	a	g	a	t	g	c	t	g	t	g	T	g	t	c	c	c	c	c	a	g	g	g	g	c	a	g	g	g	g	g	c	t	g	c	c	t
K	K	M	L	P	V	C	P	P	G	A	G	G	L	P																								
K	K	M	L	P	V	C	P	P	G	A	G	G	L	P																								
K	K	M	L	P	V	R	P	P	G	A	G	G	L	P																								
-	-	L	L	-	-	-	-	-	-	-	-	-	G	G	S	-																						
a	a	a	a	g	a	t	g	c	t	g	t	g	C	g	t	c	c	c	c	c	a	g	g	g	g	c	a	g	g	g	g	g	c	t	g	c	c	t

Fig. 4B

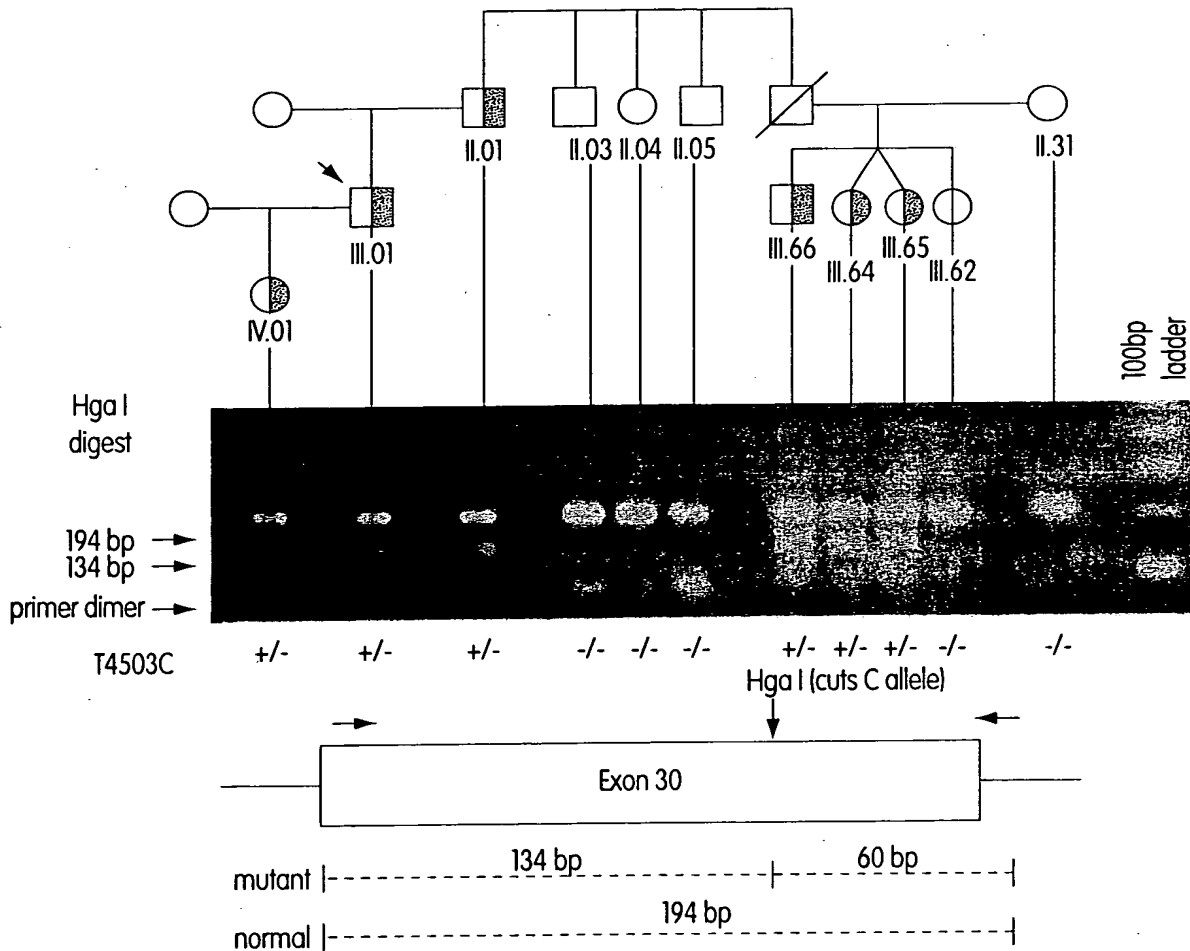


Fig. 4C



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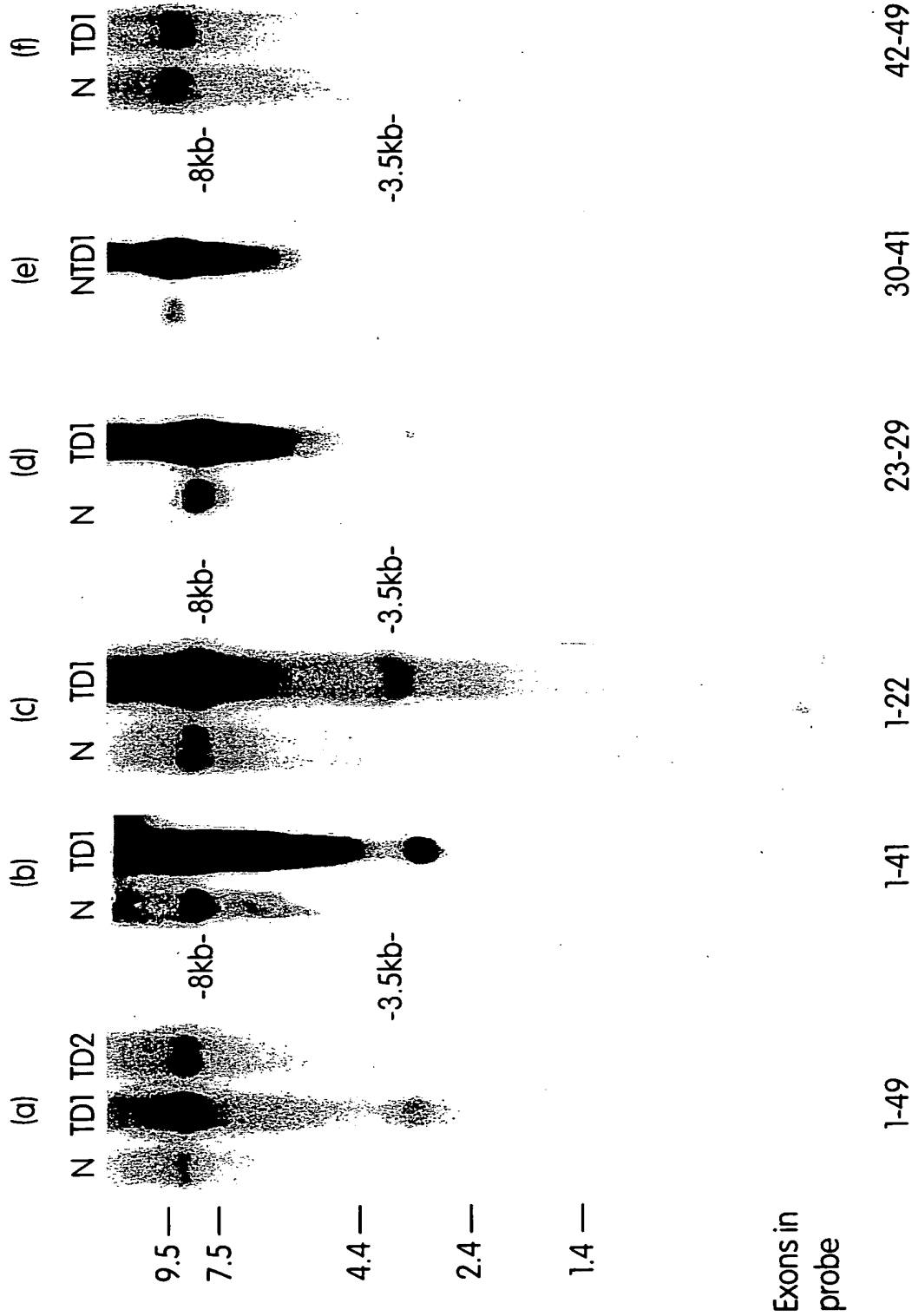
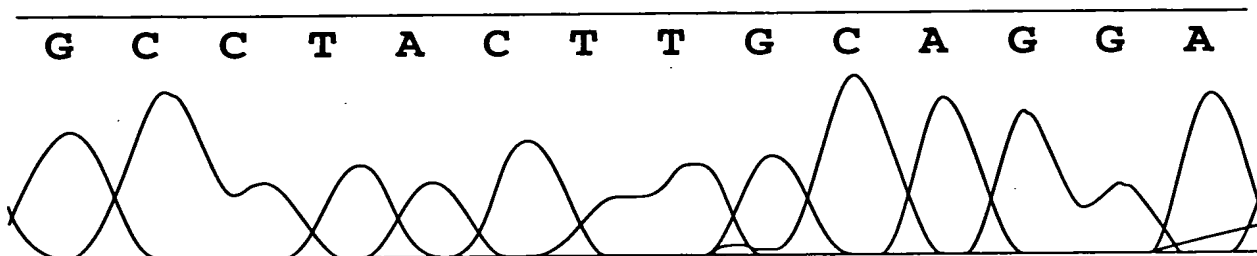


Fig. 4D

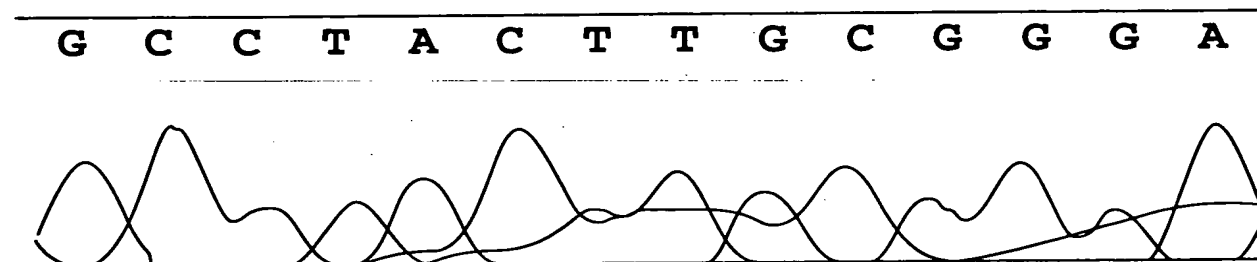


EXON 13 MUTATION:

CONTROL



FAMILY TD - 2, patient IV:10



1854

A1864G (Q597R)

1876

Fig. 5A



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EXON 13
TD-2

wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient

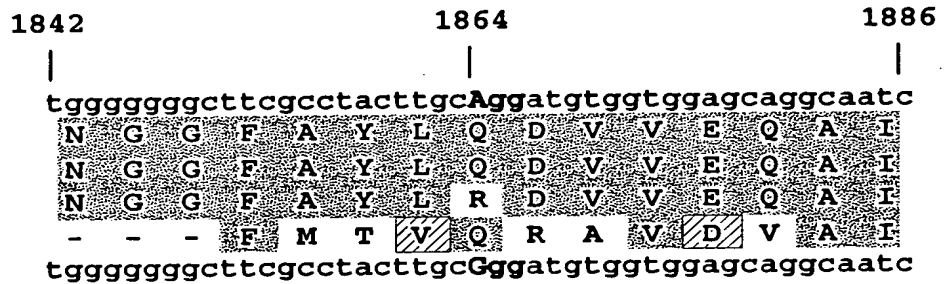
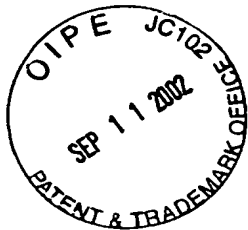


Fig. 5B



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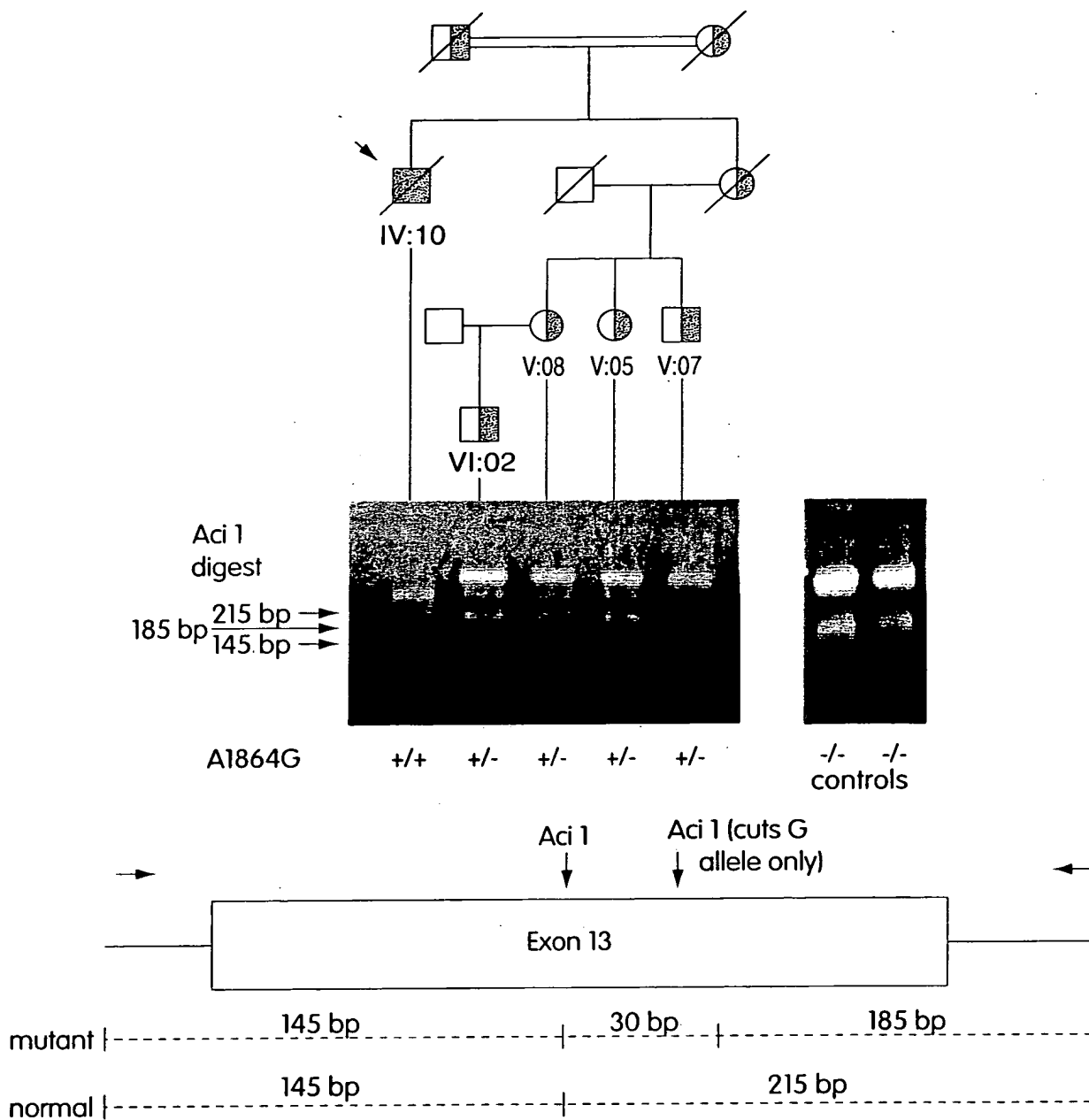


Fig. 5C



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Exon 14: FHA - 1, patient III:01

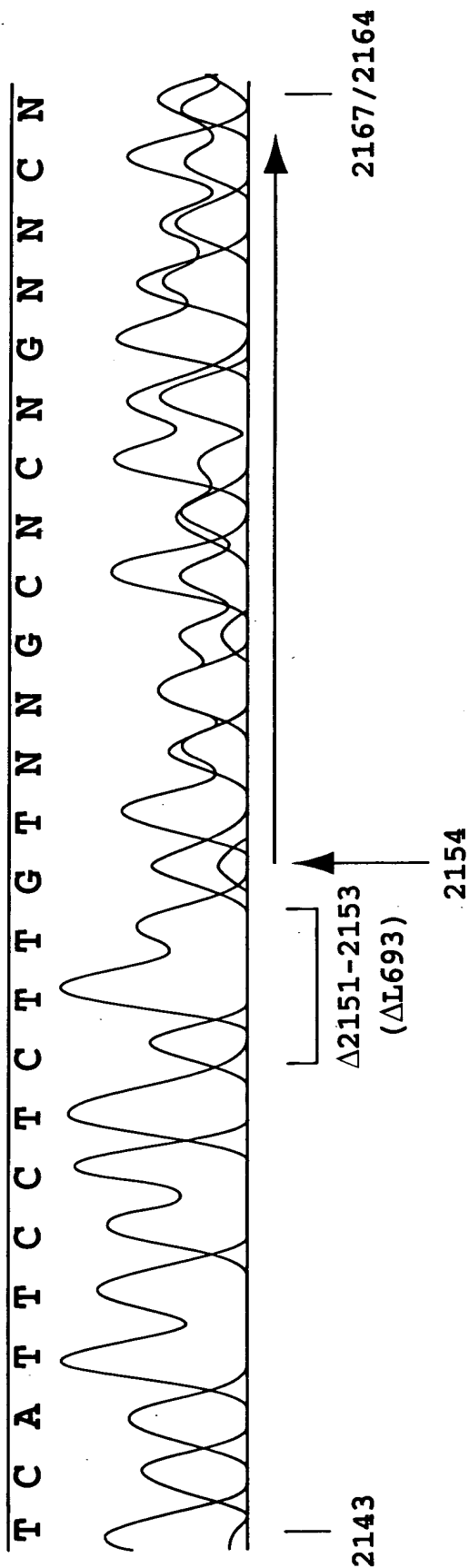


Fig. 6A



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EXON 14
FHA-1

wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient

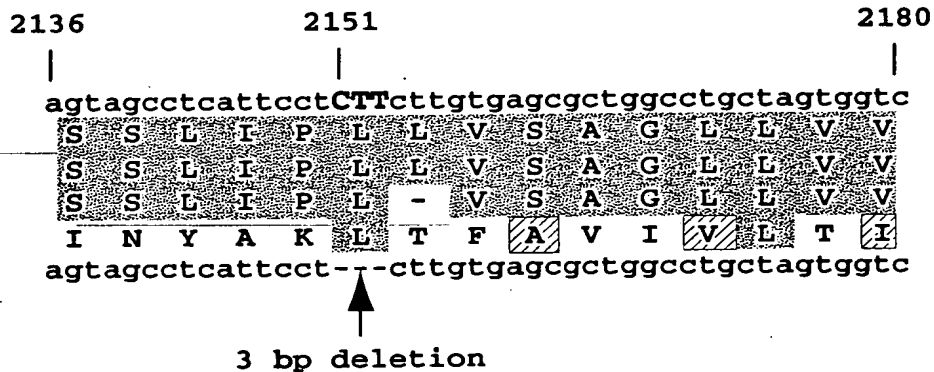


Fig. 6B

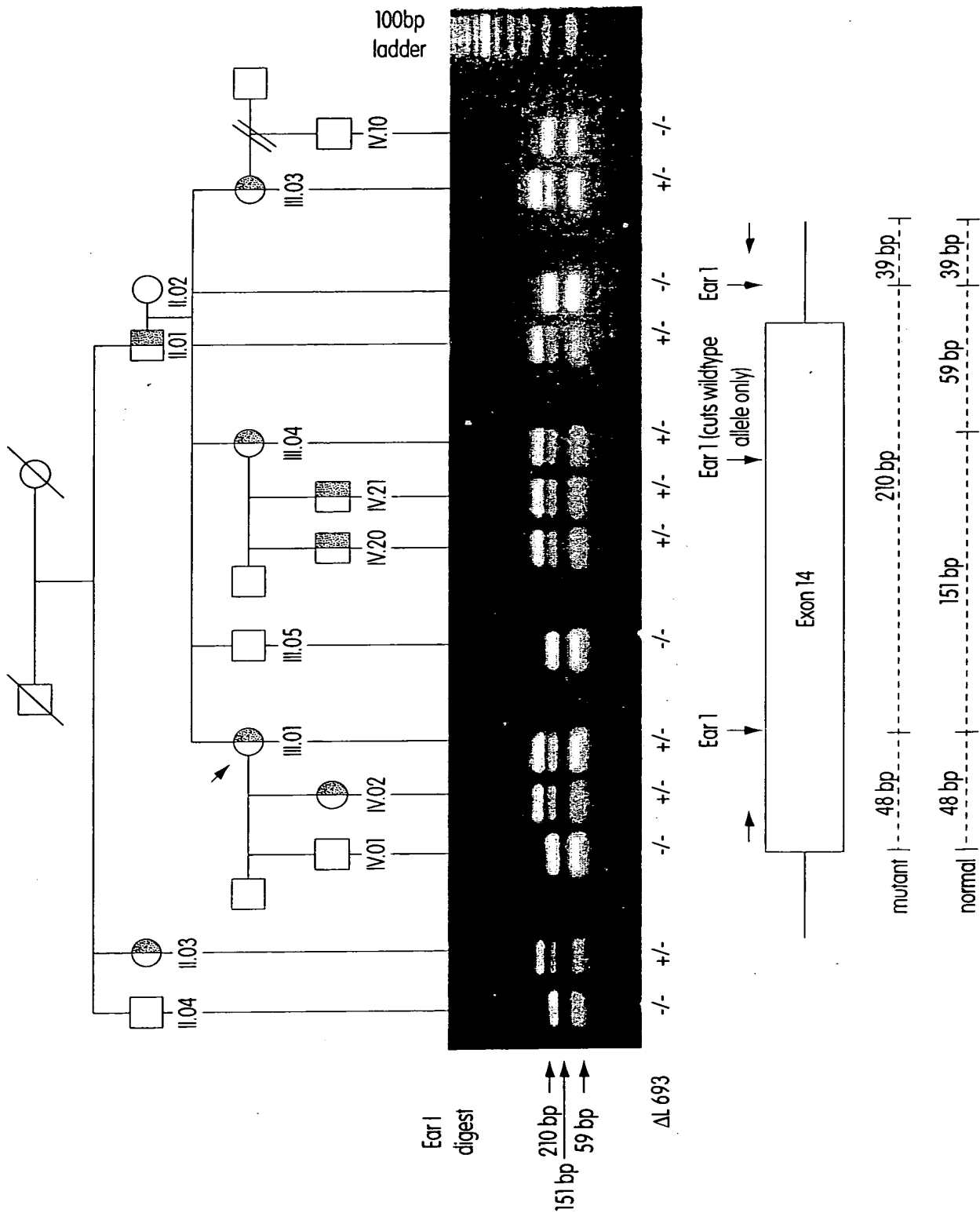


Fig. 6C



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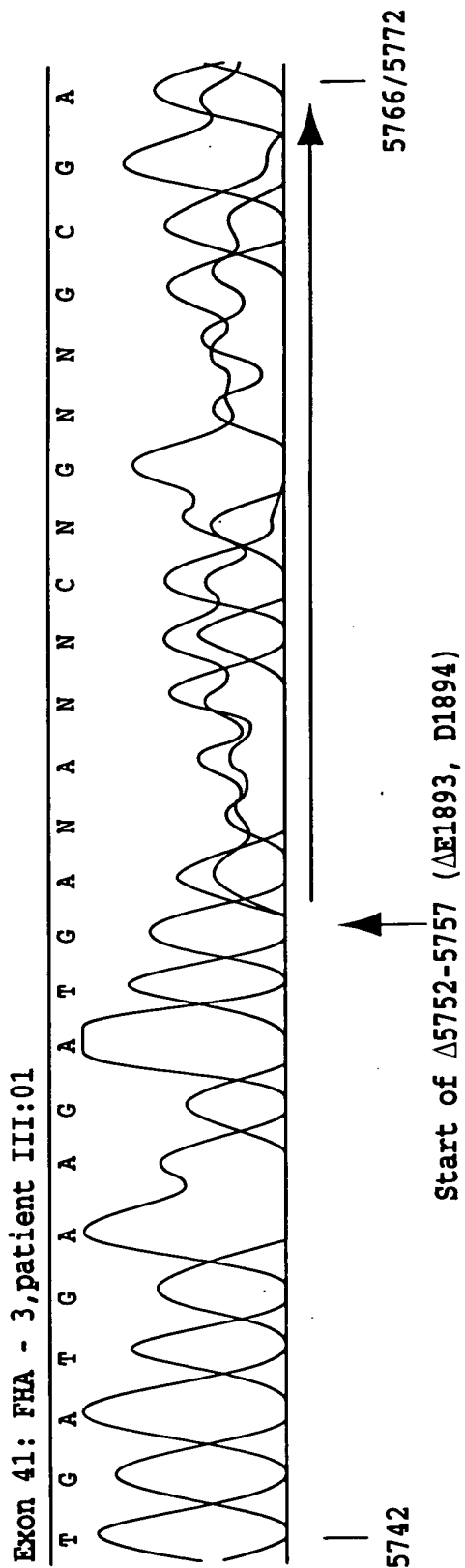
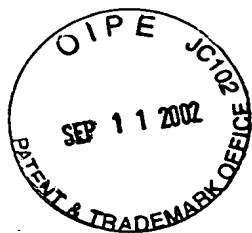


Fig. 6D



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EXON 41
FHA-3

wt sequence

HUMAN_ABC1

MOUSE_ABC1

Patient (Δ E1893, D1894)

CAEEL_ABC

Δ 5752-5757

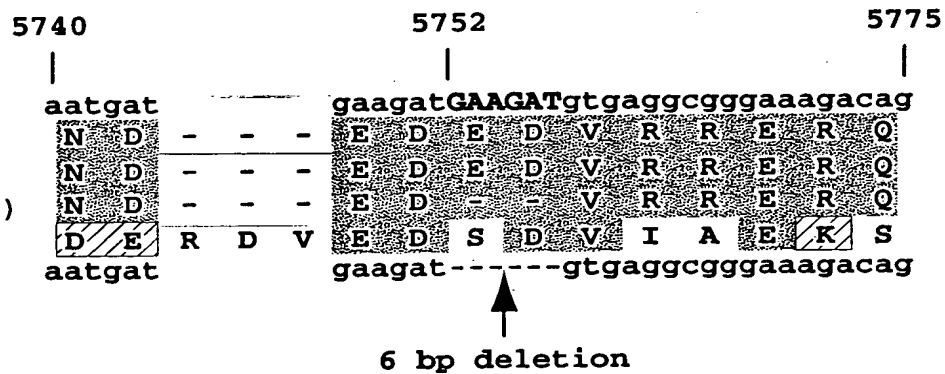


Fig. 6E



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Exon 48 mutation:

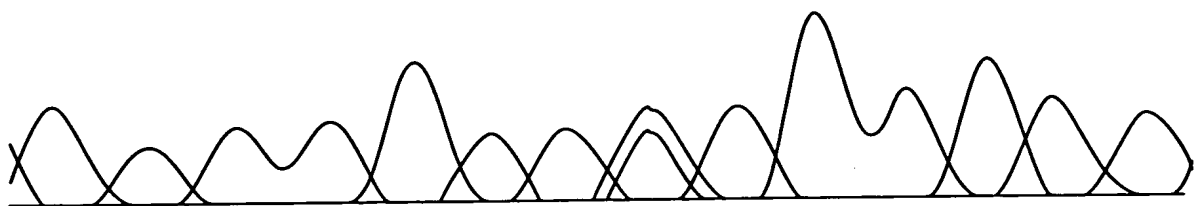
Control

A G T T G T A C G A A T A G



Family FHA - 2, patient III:01

A G T T G T A N G A A T A G



6497

C6504T (Arg2144STOP)

6510

Fig. 6F

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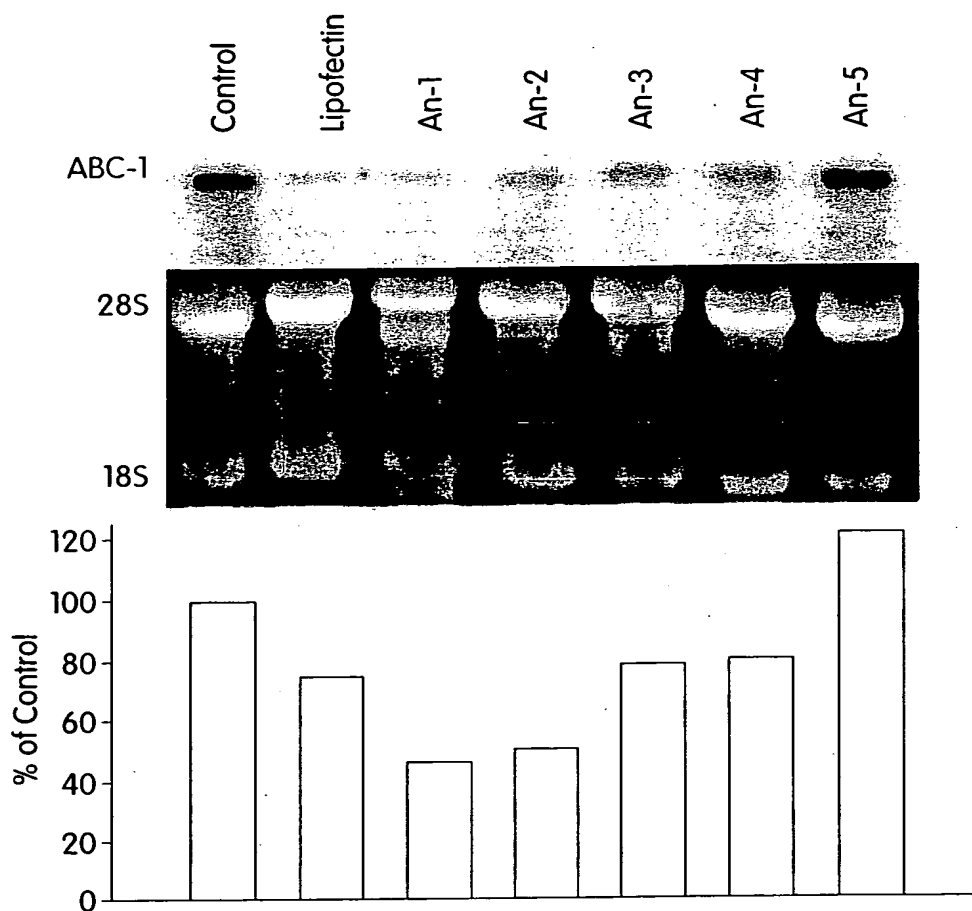


Fig. 7A

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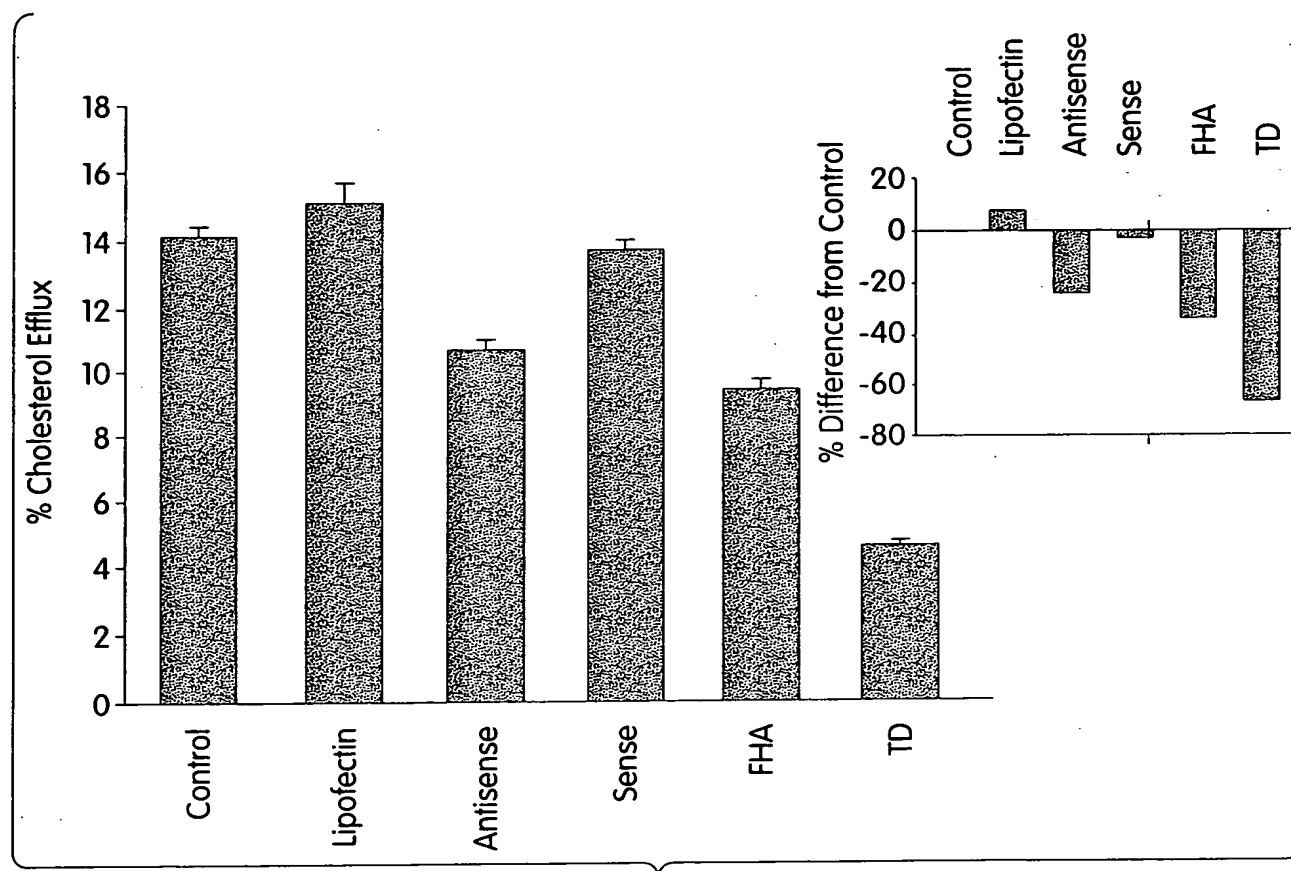


Fig. 7B



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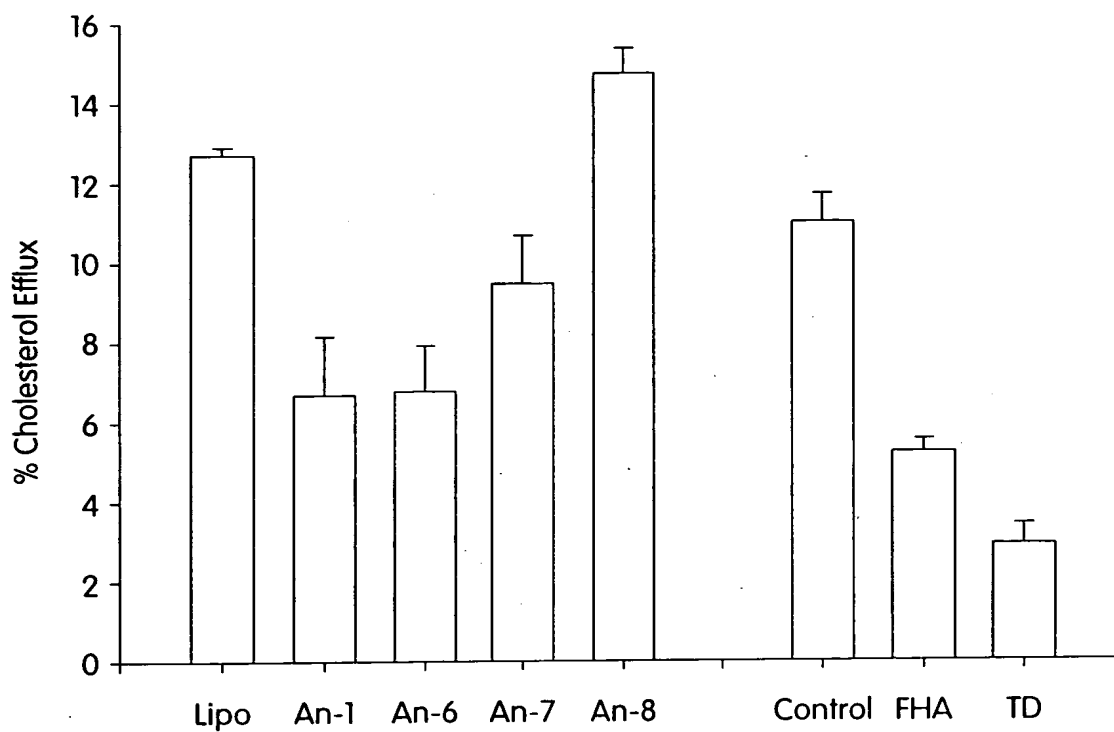
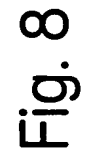


Fig. 7C



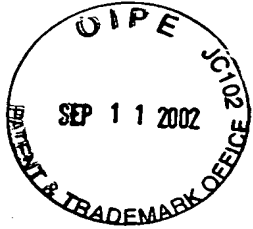


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LCGLPREKLAEEVRLSRNMDILKPIRLTLNSTSPFPSKELAEATKTLHSLGTLAQELFSMRSWSDMRQE
VMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNGTEEDAETFYDNSTTPYC
NDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWHEELSPKIWTF
MENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTQAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRT
ISRFMECVNLNKLLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVYKIRMDIDNVERTNK
IKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQMPYPCYVDDIFLRVMSRS
MPLFMTLAWIYSVAVIIKGIYVEKEARLKETMRIMGLDNSILWFSWFISLIPLLVSAGLLVVILKLGNNL
PYS DPSVVFVFLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKI FASL
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QSCLRPFTEDDAADPNDSIDIPESRETDLGSGMDGKGSYQVKGWKL TQQQFVALLWKRLLIARRSRKGFFA
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NTADILQDLTG RNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKHL
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IGGPPVVFLDEPTTGMDPKARRFLWNCALS VVKEGRSVVLTSHSMEECEALCTMAIMVNGRFRCLGSVQH
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Fig. 9A



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SEQ ID NO: 2

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TCCTGATCCTGATCTCTGTTCCGGCTGAGCTACCCACCCCTATGAACAACATGAATGCCATT
TTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTA
ATGCCAACAACCCCTGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAA
ACTTTAACAATCCATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACA
GCCAGAAAGACACCAGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCA
AGAAATCCAGCTCAAACCTGAAGCTTCAAGATTTCCCTGGTGGACAATGAAACCTTCTCTG
GGTTCCTGTATCACAACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTG
ATGTCATTCTCCACAAGGTATTTTTCGAAGGCTACCAGTTACATTTGACAAGTCTGTGCA
ATGGATCAAAATCAGAAGAGATGATTCAACTTGGTGACCAAGAAGTTCTGAGCTTTGTG
GCCTACCAAGGGAGAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCC
TGAAGCCAATCCTGAGAACACTAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCTG
AAGCCACAAAAACATTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTTCAGCATGA
GAAGCTGGAGTGACATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCT
CCTCCACCCAAATCTACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGG
GGCTGAAGATCAAGTCTCTCAACTGGTATGAGGACAACAACCTACAAAGCCCTCTTTGGAG
GCAATGGCACTGAGGAAGATGCTGAAACCTTCTATGACAACCTCTACAACCTCTTACTGCA
ATGATTTGATGAAGAATTTGGAGTCTAGTCTCTTTCCCGCATTATCTGGAAGCTCTGA
AGCCGCTGCTCGTTGGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCA
TGGCTGAGGTGAACAAGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGCATGT
GGGAGGAAGTCAAGCCCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTG
TCCGGATGCTGTTGGACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCT
TAGATTGGACAGCCCAAGACATCGTGGCGTTTTTGGCCAAGCACCAGAGGATGTCCAGT
CCAGTAATGGTTCTGTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCCAGGCAATCC
GGACCATACTCGCTTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAG
AAGTCTGGCTCATCAACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTA
TTGTGTTCACTGGAATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGA
TCCGAATGGACATTGACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACC
CTGGTCTCGAGCTGACCCCTTTGAGGACATGCGGTACGCTGCGGGGGCTTCGCCTACT
TGCAGGATGTGGTGGAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAAGT

Fig. 9B



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GTGTCATATATGCAACAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGA
TGAGCCGGTCAATGCCCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCA
TCAAGGGCATCGTGATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCC
TGGACAACAGCATCCCTCTGGTTTAGCTGGTTTCATTAGTAGCCTCATTCCTCTTCTTGTGA
GCGCTGGCCTGCTAGTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCA
GCGTGGTGTGTTGCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGA
TTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCA
CGCTGTACCTGCCCTACGTCCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCA
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TTTTTGAGGAGCAGGGCATTTGGAGTGAGTGGGACAACCTGTTTGAGAGTCTGTGGAGG
AAGATGGCTTCAATCTCACCCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATG
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GGTATTTTCTTGCACCAAGTCTTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACC
CTGGTTCCAACCAGAAGAGAAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGA
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TCGATGGCCTGGCACTGAATTTTTATGAGGGCCAGATCACCTCCTTCCCTGGGCCACAATG
GAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGCA
CCGCCTACATCCTGGGAAAAGACATTCCGCTCTGAGATGAGCACCATCCGGCAGAACCTGG
GGGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTGCAAGAACACATCTGGT
TCTATGCCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGG
CCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTG
GAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTCAATC
TGGATGAACCCACAGCTGGTGTGGACCTTACTCCCGCAGGGGAATATGGGAGCTGCTGC
TGAAATACCGACAAGGCCCGACCATTAATCTCTCTACACACCACATGGATGAAGCGGACG
TCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCC
TGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGG
AATCCTCCCTCAGTTCTTGAGAAACAGTAGTAGCACTGTGTACATACCTGAAAAAGGAGG
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TGACCATCGATGTCTCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCCGGC
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GGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGCGGGCCTTCG
GGGACAAGCAGAGCTGTCTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATT

Fig. 9C



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CTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGT
CCTACCAGGTGAAAGGCTGGAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGA
GACTGCTAATTGCCAGACGGAGTCGGAAGGATTTTTGTCTCAGATTGTCTTGCCAGCTG
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GCCTGGAACCTCAGCCCTGGATGTACAACGAACAGTACACATTTGTGCAATGATGCTC
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CCCGCTGTATGGAAGGAAACCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGT
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TCCTTCAGGACCTGACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGTATGTGCAGA
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AACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACA
GCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATA
ACAAGGGCTGGCATGCAATCAGCTCTTCTGAATGTCATCAACAATGCCATTCTCCGGG
CCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCC
TGAATCTACCAAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGGATGTCC
TTGTGTCCATCTGTGTCATCTTTGCAATGTCTTCGTCCCAGCCAGCTTTGTGCTATTCC
TGATCCAGGAGCGGGTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTG
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CCTCCTTTGTGTTCAAGATCCCCAGCACAGCCTATGTGGTGTCTACCAGCGTGAACCTCT
TCATTGGCATTAAATGGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCCGACAATAAGC
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GGCGGGAAGACAGAGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGG
AGTTGACGAAGATATATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCA
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TCAAGATGTTAACAGGAGATACCACTGTTACCAGAGGAGATGCTTTCTTAAACAAAATA

Fig. 9D

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GTATCTTATCAAACATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATG
CCATCACAGAGCTGTTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAG
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GATGTTTATCTGACACAAGTGATTATTTCTGGCTTTTTTGAATTAATCTAGAAAATGAAA

Fig. 9E



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Exon	Exon Forward Primer (bp)	SEQ ID No.	Reverse Primer	SEQ ID No.	intron(kb)	intron (kb)
exon 1	140 GGCTGGATTAGCAGTCTCTCA	70	ATCCCCAACTCAAAACCACA	119	intron 1	>6.413
exon 2	94 GGATTTCCAGATCCCAAGTG	71	AAGTCCAATTTAGCCCAAGTT	120	intron 2	>4.241
exon 3	142 GACAGACTTGGCATGAAGCA	72	CCAGCCATTCAAAATTTCTCC	121	intron 3	>1.248 (1.6)
exon 4	119 GCAGTGGCAGTCACTTCTG	73	GGGTGCAGGTCAATTTCCAAT	122	intron 4	>1.512
exon 5	122 CGTTTCTCACTGTCCCAAT	74	CCCCCTCACCCACCAATTACAA	123	intron 5	>1.796 (3)
exon 6	177 ACTTCAAGGACCCAGCTTCC	75	TGTCCAAGGAAAGCCCTCAC	124	intron 6	>2.726 (10)
exon 7	93 TCGGTTTCTTGTGTTAAACTCA	76	AGGACCTCTTGCCAGACTCA	125	intron 7	4.975
exon 8	241 TCCCAAGGCTTTGAGATGAC	77	AGGAGATGACACAGGCCAAG	126	intron 8	>2.311 (.5)
exon 9	140 GGCTCCAAAGCCCTTGTA	78	CGCACACTCTGAAGCTACC	127	intron 9	0.332
exon 10	117 GCTGCTGTGATGGGTATCT	79	ACCTCACTCACACCCTGGAA	128	intron 10	4.208
exon 11	198 TTTGTAAATTTGTAGTGTCTCTCA	80	GCCTCTGCCTGAACCTTAT	129	intron 11	0.747
exon 12	206 TAGTCAGCCCTTGCCTCCTA	81	CAAAATCATGACACCAAGTTGAG	130	intron 12	0.523
exon 13	177 AAAGGGCTTGGTAAGGTA	82	CATGCACATGCACACACATA	131	intron 13	1.787
exon 14	223 GATGTGGTGTCTCTCTAGC	83	CCTTAGCCCGTGTGAGCTA	132	intron 14	1.747
exon 15	222 CAAGTGAGTGTGGGATTG	84	TGCTTTTATTCAGGGACTCCA	133	intron 15	1.059
exon 16	205 GCAATTCAAATTTCTCCAGG	85	CCCATGCACTGCAGAGATTTC	134	intron 16	1.105
exon 17	114 TCAAGGAGGAATGGACCTG	86	AAGGCAGGAGACATCGCTT	135	intron 17	1.789
exon 18	172 CTGAAGTTCAAGCGCAGTG	87	GGGATCAGCATGGTTTCTTA	136	intron 18	0.99
exon 19	132 TGCAGACTGAATGGAGCATC	88	GCTTAAGTCCCACTCCTCCC	137	intron 19	1.307
exon 20	143 GCCAGGGGACACTGTATTCT	89	ATTTTCTCCGCATGTGTGT	138	intron 20	0.204
exon 21	138 AGGTCTCTGCTTCACTCA	90	TCACAGAAGCCTAGCCATGA	139	intron 21	0.706
exon 22	221 CCAGTGTCTACCCCTGCTAA	91	AACAGAGCAGGAGATGGTG	140	intron 22	>0.866 (1.7)
exon 23	73 CACACACAGAGTCTTTGGA	92	TCTGCACCTCTCCTCCTCTG	141	intron 23	0.986
exon 24	203 ACCTGGAACAGGTGTGGTGT	93	ACTGGGGCCCAACATTATCA	142	intron 24	1.668
exon 25	49 GGGCTAACATGCCCACTCAGTA	94	CTTCCCATCTGCAACAAAC	143	intron 25	0.196

Fig. 10 (SHEET 1 OF 2)



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exon 26	114	GTTTGTTCAGATGGGGAAG	144	GCTAAGGCCCATCCAAAGAA	intron 26	326	1.396	1.4
exon 27	149	CACCAGAAGAGGAGCATGG	145	TCAAGTGCATCTGGGCATAA	intron 27	327	1.649	1.6
exon 28	125	CTGGACTCGTAGGGATTGCG	146	TCTGAAGTCCATTCCCTTGG	intron 28	328	>0.728(1.4)	1.4
exon 29	99	GCCTGTTCACAGAGAAATGCTT	147	CAATGTGGCATGCAGTTGAT	intron 29	329	>2.589(3)	3
exon 30	190	TTACGGAAATGATCCTGTGCTC	148	GAAGCTACAGCCCATCCT	intron 30	330	1.521	1.5
exon 31	95	AGTCAGGTTTCCGGTCACAC	149	CATTTCCCTCCACTGTTTCAG	intron 31	331	>0.944(\)	>0.9
exon 32	33	CCGTTCCCTTATATCCTCAGTG	150	CCAAGGCTTTTCAATCCA	intron 32	332	>1.062(/6.5)	>1.0
exon 33	106	CCTGTACACACTCGCACCTGA	151	GATCCGTTTAACTGCAAC	intron 33	333	1.475	1.5
exon 34	75	TGTTGTCCACAGGTTCAGAA	152	ATGCCCTGCCAATTTTAC	intron 34	334	0.522	0.5
exon 35	170	TGAGGTTTATGGGCATGGTT	153	CTCTGCAGCTGTTCCCTTAC	intron 35	335	1.228	1.2
exon 36	178	ATGTTTTTCTTGGCTGTGC	154	TATCAATCCATGGCCCTGAC	intron 36	336	>1.898(2)	2
exon 37	116	ATCTGCCCTTCTTGTCTGA	155	AGAGTCCTGCCCTCCTTCT	intron 37	337	0.112	0.1
exon 38	145	AGGAGCTGCACAGTGGATA	156	AAGGCAGTCAGCAGTGTCAA	intron 38	338	1.545	1.5
exon 39	124	TCACCTCCCATATTCAGAACTTGA	157	GGGGAACATCCTGTGCTTAG	intron 39	339	1.087	1.1
exon 40	130	TGTTTATTGGAAGATCGGTGAA	158	CCATTGGTGAGTGTTCCTT	intron 40	340	0.265	0.3
exon 41	121	CGTTAGAGACTGAATCTTTGTCTG	159	AGTCAGCAAACTGCTGGGT	intron 41	341	>0.622(0.9)	0.9
exon 42	63	AGTCCTGCCCTCCACAGTTG	160	ATTGCTCCATCCTGGCATAA	intron 42	342	0.909	0.9
exon 43	107	GGTAGTTACGTGTAGGGCA	161	TCATGGATGATTTTATGTGCTTC	intron 43	343	2.355	2.4
exon 44	142	CAGGAACATTAGCCAGATTG	162	GCGTGTGGAAGCCATAAG	intron 44	344	0.372	0.4
exon 45	135	CATGTATGTGTAGACAGCATGA	163	GCCAACTACAAACAGCCCT	intron 45	345	>1.059(1.3)	1.3
exon 46	104	CTGTTTCAAAGATGCTTCTGC	164	TGATCGCATATTTCTACTTGGAAA	intron 46	346	0.483	0.5
exon 47	93	CCTAGGAAGCTGGAATGCTG	165	TCCCTTTTATTTTAGAGGCACCA	intron 47	347	0.659	0.7
exon 48	244	GGTTCCCGGTTTCAGTAT	166	GATCAGGAATTCAGCACCAA	intron 48	348	0.941	0.9
exon 49	295	CTTGACCTTAATTTCAACATCTGG	167	TGGGTTCCATAATAGAGTTTCACA			>1.075	

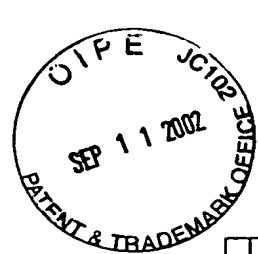
Fig. 10 (SHEET 2 OF 2)



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ERRORS IN PUBLIC SEQUENCE (differences between samples and Genbank entry AJ012376.1):				
Exon/Intron	Nucleotides	Amino Acid Change	Sequence difference/context	SEQ ID NO:
2	T150C A152G	no change	Public sequence: TGTCAGCTGTACTGGAAGTGG	168
			Correct sequence: TGTCAGCTGCTGCTGGAAGTGG	169
7	C839T	no change	Public sequence: AGGAGCTGGCCGAAGCCACAA	170
			Correct sequence: AGGAGCTGGCTGAAGCCACAA	171
33	C4738T	T1495I	Public sequence: AATGATGCCACCAACAATG	172
			Correct sequence: AATGATGCCATCAACAATG	173
35	C5017T	P1588L	Public sequence: GAGTGGCTCCGATGACCACA	174
			Correct sequence: GAGTGGCTCTGATGACCACA	175
43	G5995A	R1914K	Public sequence: TTCCTTAACAGAAATAGTATC	176
			Correct sequence: TTCCTTAACAAAAATAGTATC	177
48	C6577T	P2108L	Public sequence: GGAAGTGTCCAAAAGAGAAA	178
			Correct sequence: GGAAGTGTCTTAAAAGAGAAA	179
49	G6899A	not applicable	Public sequence: AGTAAAGAGGGACTAGACTTT	180
			Correct sequence: AGTAAAGAGGAAC TAGACTTT	181
Mutations:				SEQ ID NO:
13	A1864G	Q597R	More common: GCCTACTTGCAGGATGTGGTG	182
			Less common: GCCTACTTCCGGGATGTGGTG	183
14	delta CTT 2151-3	delta L093	More common: CCTCATTCCTCTTCTTGTGACGG	184
			Less common: CCTCATTCCT/CTTGTGACGG	185
15	G2385A	V771M	More common: GCAGGACTACGTGGGCTTCAC	186
			Less common: GCAGGACTACATGGGCTTCAC	187
18	C2799T	R909Stop	More common: AAAAGTCTACCGAGATGGGAT	188
			Less common: AAAAGTCTACTGAGATGGGAT	189
18	C2860T	T929I	More common: GGCCAGATCACCTCTTCTCTG	190
			Less common: GGCCAGATCATCTCTTCTCTG	191
22	T3346C	M1091T	More common: ACACACCATGGATGAAGCG	192
			Less common: ACACACCAACGGATGAAGCG	193

Fig. 11 (SHEET 1 OF 4)



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Intron 24	(+1) G to C splice donor site	Altered transcript length	More common: Less common:	CCTGGAAGAGTAAGTTAAGT CCTGGAAGAGTAAGTTAAGT	194 195
30	T4503C	C1477R	More common: Less common:	GCTGCCCTGTGTCTCCCCAGG GCTGCCCTGTGTCTCCCCAGG	196 197
35	GG 4958-57 to C	frameshift at aa 1628	More common: Less common:	TAGCCATTATGGAATTACTGCT TAGCCATTATCAATTACTGCT	198 199
41	delta AAGATG 5752-7	delta(E.D)1893-1894	More common: Less common:	GATGAAGATGAAGATGTGAGCGCGGA GATGAAGATG/TGAGCGCGGA	200 201
48	C6504T	R2144Stop	More common: Less common:	AATAGTTGTACGAATAGCAGG AATAGTTGTATGAATAGCAGG	202 203
Promoter Variants: Location	Position Relative to Xenon cDNA	Position Relative to SEQ ID NO: 14 Containing Exon 1			SEQ ID NO:
1	G57C	8216	More common: Less common:	ACACGCTGGGGTGTCTGGCTG ACACGCTGGGGTGTCTGGCTG	204 205
5	(-)4 ins. G	8158	More common: Less common:	GACCAAGCACGGCTCCCTG GACCAAGCACGGCTCCCTG	206 207
5	A (-)380 G	7780	More common: Less common:	CATTTTCTTAGAAAAGAGAGGT CATTTTCTTAGAAAAGAGAGGT	208 209
5	A (-)479 C	7681	More common: Less common:	GAAAATTAGTATGTAAAGGAAG GAAAATTAGTCTGTAAAGGAAG	210 211
5	A (-)738 G	7422	More common: Less common:	CCTCCGCTGCCAGGTTACGGATT CCTCCGCTGCCGCGTTACGGATT	212 213
5	A (-)1045 G	7115	More common: Less common:	TATGTGCTGACCATGGGAGCTTGT TATGTGCTGACCGTGGGAGCTTGT	214 215
5	A (-)1113 G	7047	More common: Less common:	GTGACACCCAAACGGAGTAGGG GTGACACCGAGCGGAGTAGGG	216 217
5	(-)1181 ins. CCTT	6979	More common: Less common:	AGTATCCCT/TGTTACAGGAA AGTATCCCTCCCTTGTTCACGAGAA	218 219

Fig. 11 (SHEET 2 OF 4)



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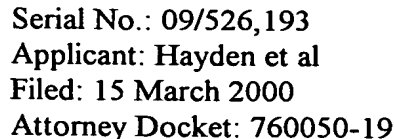
Polymorphisms:					
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5	G548A	no change	More common:	CTGGGTTCCTGTATCACAACC	220
			Less common:	CTGGGTTCCTATATCACAACC	221
6	G730A	R219K	More common:	GGCCTACCAAGGGAGAAACTG	222
			Less common:	GGCCTACCAAGGAGAAACTG	223
Intron 7	G(+)/2383 T	Not applicable	Allele 1:	TTTAAAGGGGGTGTATTAGGA	224
			Allele 2:	TTTAAAGGGGTGTATTAGGA	225
Intron 7	G(+)/3035 T	Not applicable	Allele 1:	GAAGAAATTTGTTTTTTGATT	226
			Allele 2:	GAAGAAATTTTTTTTTTGATT	227
8	C1010T	no change	More common:	GCGGGCATCCCGAGGGAGGGG	228
			Less common:	GCGGGCATCTGAGGGAGGGG	229
8	G1022A	no change	More common:	AGGGAGGGGGCTGAAGATCA	230
			Less common:	AGGGAGGGGACTGAAGATCA	231
Intron 9	(-)/42 ins. G	Not applicable	More common:	AGGAGCCAAACGCTCATTTGT	232
			Less common:	AGGAGCCAAAGCGCTCATTTGT	233
Intron 13	T(+)/24 A	Not applicable	More common:	AAGCCACTGTTTTTTAACCAGT	234
			Less common:	AAGCCACTGTATTTAACCAGT	235
15	A2394C	T774P	More common:	CGTGGGCTTCACACTCAAGAT	236
			Less common:	CGTGGGCTTCCCACTCAAGAT	237
15	G2402C	K776N	More common:	TCACACTCAAGATCTTCGCTG	238
			Less common:	TCACACTCAACATCTTCGCTG	239
Intron 14	C(+)/16 T	Not applicable	Allele 1:	GCAGCCTCACCGGCTCTTCCC	240
			Allele 2:	GCAGCCTCACTCGGCTCTTCCC	241
17	A2723G	I883M	Allele 1:	AGAAGAGAATATCAGAAATCT	242
			Allele 2:	AGAAGAGAATGTCAAGAAATCT	243
Intron 17	C(+)/2000 G	Not applicable	Allele 1:	GCGCAGTGCCTGTGTCTCTTA	244
			Allele 2:	GCGCAGTGCCTGTGTCTCTTA	245

Fig. 11 (SHEET 3 OF 4)



21	T3233G	no change	More common: Less common:	GATCTAAGGTTGTCATCTCTGG GATCTAAGGTTGTCATCTCTGG	246 247
Intron 21	G(+118 T	Not applicable	Allele 1: Allele 2:	CTCTCTCTCTTAGGACAGAAGAGA CTCTCTCTCTTAGGACAGAAGAGA	248 249
Intron 21	A(+1563 G	Not applicable	Allele 1: Allele 2:	CATTCTAGGGATCATAGCCAT CATTCTAGGGATCATAGCCAT	250 251
Intron 24	G(+1321 T	Not applicable	Allele 1: Allele 2:	AAGTACAGTGGGAGGAACAGCG AAGTACAGTGGGAGGAACAGCG	252 253
Intron 29	A(-1624 G	Not applicable	Allele 1: Allele 2:	AATTCTTAAAAATAGAAATGCA AATTCTTAAAAATAGAAATGCA	254 255
Intron 31	T(+130 C	Not applicable	More common: Less common:	GGCCCCGCTTATTATTACT GGCCCCGCTTATTATTACT	256 257
Intron 33	A(+1732 G	Not applicable	Allele 1: Allele 2:	TGAGAGAAATTAATGACCCCG TGAGAGAAATTAATGACCCCG	258 259
Intron 33	C(+1898 T	Not applicable	Allele 1: Allele 2:	TTTGCTGAAACAATCACTGCA TTTGCTGAAACAATCACTGCA	260 261
Intron 34	C(+1234 T	Not applicable	Allele 1: Allele 2:	AACCTCAGTCCCTCATCTGTG AACCTCAGTCCCTCATCTGTG	262 263
34	G4834A	R158TK	More common: Less common:	CTGGACACCAAGAAATATGTC CTGGACACCAAGAAATATGTC	264 265
37	C 5266G	S1731C	More common: Less common:	TCCTATGTCCTCCACCAAT TCCTATGTCCTCCACCAAT	266 267
Intron 43	T(+118 C	Not applicable	More common: Less common:	AAGAAGTGGCTGTATTTTGC AAGAAGTGGCTGTATTTTGC	268 269
Intron 43	C(+1665 G	Not applicable	Allele 1: Allele 2:	AACTGATTTGATTTGGTATAGCTG AACTGATTTGATTTGGTATAGCTG	270 271
48	C6521T	no change	More common: Less common:	CAGGGTCCAAACCCGGACCTGA CAGGGTCCAAACCCGGACCTGA	272 273
Intron 10	(+114 ins. T	Not applicable	More common: Less common:	GGTCAGGGATGGGGACAG GGTCAGGGATGGGGACAG	284 285
Exon 16	G2547A	V8251	More common: Less common:	CCACTTCGGTCTCCCATG CCACTTCGATCTCCCATG	286 287
Polymorphism in an ABC1 BAC contig: This polymorphism is within approximately 200Kb of the ABC1 gene					SEQ ID NO:
	A or G	Not applicable	Allele 1: Allele 2:	TTGGGAGGCTAAGGCAGGAGAA TTGGGAGGCTAAGGCAGGAGAA	274 275

Fig. 11 (SHEET 4 OF 4)



Genomic contig containing ABC1 exon 1:

Underline = putitive promotor element

Fig. 12 (SHEET 1 OF 32)

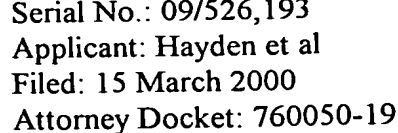


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Fig. 12 (SHEET 3 OF 32)



SEQ ID NO: 15

[illegible]

Fig. 12 (SHEET 4 OF 32)



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Fig. 12 (SHEET 5 of 32)

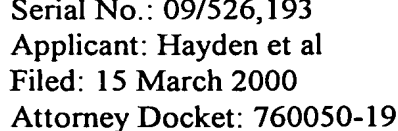
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SEQ ID NO 16

Genomic contig containing ABC1 exon 3:

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Fig. 12 (SHEET 6 OF 32)



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Fig. 12 (SHEET 7 OF 32)



SEQ ID NO 17

Genomic contig containing ABC1 exon 4:

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Fig. 12 (SHEET 8 OF 32)



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SEQ ID NO 18

Genomic contig containing ABC1 exon 5:

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SEQ ID NO 19

Genomic contig containing ABC1 exon 6:

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Fig. 12 (SHEET 10 OF 32)



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SEQ ID NO 20

Genomic contig containing ABC1 exon 8:

ccgtttggcaaatgctcagtaaaagaaaagggttagaaggggagaaaggcattttatcccaagccttcaggaatcaggat
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Fig. 12 (SHEET 11 OF 32)



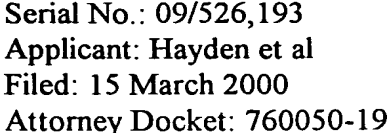
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Fig. 12 (SHEET 12 OF 32)



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Fig. 12 (SHEET 13 OF 32)



SEQ ID NO 21

Genomic contig containing ABC1 exon 9 through 22:

Fig. 12 (SHEET 14 OF 32)



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Fig. 12 (SHEET 16 OF 32)



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tccaggtgagtgccgagctgacttcttgggtggacgtgctgtggggacagcccattaaagaccacatcttggggccctgaa
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SEQ ID NO: 22

Genomic contig containing ABC1 exon 23 to 28:

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gATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCCTTCGGGGACAAGCAGAGCTGTCCTTCGCCCCGTTCACTGAAGATGA
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acacggtggaat

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SEQ ID NO: 23

Genomic contig containing ABC1 exon 29:

g g g a a g c a t t t a a a a a a a a a a a g t a t a t a t a t a t a t a t a t a t a t g t a a t g t g a a t t g g c c t c t t t t t c t c t a a
g c c c a c a t t t t c t t c t t a c a t a g t t c a g g t t t a c t t t a t t t t t c c t t t c c g g c t g c t g a c c c t g t a t t g c c c g t a g t t g
t g g a a c a t a g c a t g t g t t t g t g a c c t g t g c c t g t t a t t t t t g t g c t t t c t a g t t g t g c a t g c a a a g a g t a c a a a g t t t t c
t t g c c c t t t c t t g g a a a t c c t g c t t g t c t g t g c c a a g g g a t a a t t g t g a a g c a c t t t t g a a a t a c t t a a t g a g t t g a
t t t t c t t c a a a t t a a a a a a a t a t a a a t g t a t a t g t g t a t g t a c a t g t g t g t a c a c a t a c a c a c t t t a t a c a t a c a g
c c c a t t t a a a c a a g c t c c a c t t t g g a g t g c t c t a c g t c a c c c t g a t g c c g a a t a c a g g g c c a g a g t c t g a g a t c c t t c
g g g t g g t t t c t g t g t t t t g t t c a t t t c t g t t t t a a g a g c c t g t c a c a g a g a a a t g c t t c c t a a a a t g t t a a t t a t a a a
a a c a t t t t t a t c t c t c g a t t a c t g g t t t t a a t g a a t t a c t a a g c t g g c t g c c t c t c a t g t a c c c a c a g C A A T G A T G C T C C
T G A G G A C A C G G G A A C C C T G G A A C T C T T A A A C G C C C T C A C C A A A G A C C C T G G C T T C G G G A C C C G C T G T A T G G A A G G A A A C C
C A A T C C C G t g a g t g c c a c t t t a g c c a t a a g c a g g g c t t c t t g t g c t t g t t g c c t g g t t t g a t t t c t a a t a t g c t g c a t t t
a t c a a c t g c a t g c c a c a t t g t g a c c g c c a g c a t t t g c c c t t t g a a t t a t t a t t a t g t t t t a t t t a c a a a a g c g a a g g t a
g t a a c c g a a c t a a a t t a t c t a g g a a c a a c g t t t g g a g a g t c t t c t a a c a c c g y s c a a a g c a c g t c a t t a c a g a c a t t g
t t t a c t g a t t t a g a a c c t t a a t a t t t a a t t a a a t a c g c a c t t t a c a c t t a c t g a t g a a a t g c t t t t c c t t t c t t t c t c t
c c c a g c c c t g t a c t t a a g t g c t t c a a t a g g c t c t c a t t a t a t a t g a t t t t t a g g t t t t g c t t a t c a g c t t c t t c g c t t t
t a t a a t c t g a a a a g a t g g c a t a t g a a t t t t a t a a a a g g g a c a c t t t c t t c t t c t c a a a t t g t a t a t t t t t a t t g t a c t
t t c c t t c a a a a c c c c t t t t a a a a a g t a a g c a g t g g a t a a a t a a a t t c a g t g a a g c a t c c a t a t g a c c c t t a a g t g a g t g
t a g g g g a a g g g a g g t c a c c a g a t c a c t g t g a g t g a a g a t g g t g g a g a g g t g a g g a t c t t a t g a g g c c g t g c t c a a g g c t g
g t a g a g g t g g g t t a g t g t t t c c a g g t t t a g g c a g a a t c t c a g c t g a g g t c a t g a a c a a c a g t g a t c t c t g a a a a t t a t
g g c a a g g t g g g a a g g t g c t g g a g a a t t g g a g a g g g g c a a a c t t g a c t t t c a a g t t t c a a t g g g a a g a t a g g t g a c t c t g
c a c a c c a c a g a a c a g t g a g c a t g a t a a c c t g t t t a t a c a a g g t t c t a g a g c a g a t t t c t a a a t g g a t a g c t a c t g t g t g c
t t g t t t g t t c t t a a t t a g t a t t g g a t a g t t a c t a a a t a c t t g t t a g t a c t t a g t a c a t a a t g g g t g g t a a a t c c t a g c a g
c t a a t a t t g g t t c c c a a a t a a c c a g a t g a c a a g g a t a g a g a a g g a c a c a g a c a c g g c c t a t c t g g a t t t c a t g g t g c c t t
t g a t t t t c c a c a t g a a g g t t g t g t a g g g a a g a t a g a a g c a t g a g a t g a g a t g a t a a t a t a g t t a t c t g g a t t c a t c a c t g
g c c a g c t g a a c c a t a t g a a c t c a t g g a t t g a t g c t a g c t t a g g a a g g c t c t g t a g g a g c c a g a a c t g g g c t g a g a g c c a g
c c c a t a g a g a c a a a a g a g g c c c g g c c c t g a c a t c a g a g g g t t c a a c a t g a t g t c t g a g c c c c a c c t a c a g t c t g c c g g a
g g t g g t t g g a a g g a a g a g c c t t t a t c c t t a c a a t t c t t a c t g a a a t t c a a a t t t t t a g g t t t t g c a a a a a a t g g t g g a c
c t g a a g g a a a t t t g a c a g g a g c a t g t c t c a g c t g t a t t t a a a t t t g t c t c a g c c a a t c c c c t t t t g a a t g t t c a g a g t g t
a a g c t t c a g g a g g g c a g c g c t c t t a g t g t g a c t t t t c t g g t c a g t t c a g g t g c t t t a a g g a g a c a a t t a g a g a t c a a t c
t g g a a a a c t t c a t t t g a a t t t t t a a t a c a t a a g a a a a c a a t a a g a a a t a g t t a a a a t a t a t a t t t a t a t a a t a t a t a
t g t g t g t g t g t g t g t g t g t g t g t a t a t a t a t a t a t a t t t t a t t t a t t t a t t t t t t t t t g a g a t g g a g t c t c g
c t c t g t t g c c c a g g c t g g a g t g c a g t g g c t c a a t c t t g g c t c a c t g c c a c c t c t g c c t c c c a g g t t c a a g t g a t t c t c c t
a c c t c a g c c t c c t g a g t a g c t g g g a t t a c a a g c a t g t g c c a c c a c a c t g g c t a a

Fig. 12 (SHEET 22 OF 32)



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SEQ ID NO: 24

Genomic contig containing ABC1 exon 30 and 31:

tcttgccagtctctactcatttttcagcacatcgagcataagatccagactctttccaggcctctctcatctggctcct
ctcctcctcctttatcattactcttcttcgtagcttatcctactccagccatgctgtcttcttatttctctaaaaarta
gaaatgcatttcttccctagggcctttgtacctgcacttgccatcgcttttgctcagaatgttctttttgccaagcttttg
cccagcttggttctccatcattgttatgttttggtgaaatgtcttctcttagtaggttcatttctccccagtcactgtctt
tttattttgctttattttgggccatctaagggttatcttattagtgatttgttgttcgtctcctccatgggcatacacct
ccatgaaggcaggtattttcaccttaggccctcgaatatactggacagcatctggcacgtagtagatgtcaacgaatgt
ttgttgtgtgagcaaatggttggttgattggattgaactgagttcagtagttaaataatttagggcctctttgcattctat
tttacttatgtataaaatgatacataatgatgatataaatgatgtcacagtgtagaaggctgttgtgggatcaagcaatc
aaatgagatcatgcttgtcttttccaaatggtgaggggaatagatgcatgtttgtggtgttacggaatgatcctgtgctc
ctgaggcaacagaaaggccaggccatctctggtaatcctactcttgcgtcttccctttgcagAGACACGCCCTGCCAGG
CAGGGGAGGAAGAGTGGACCACTGCCCCAGTTCCCCAGACCATCATGGACCTCTTCCAGAAATGGGAACCTGGACAATGCAG
AACCTTACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCCTGTGTGTCCTCCAGGGGAGGGGGGCT
GCCTCTCCACAgtgagtcactttcagggggtgattgggcagaaggggtgcaggatgggctggttagcttccgcttggaa
gcaggaatgagtgagatatcatgttgggaggggtctgtttcagtccttttttgttttttttctgaggcggagtc
ttgctctgtcgccaggctggagtgctgtggcatgatcttgctcactgcaacctccacctcccagggtcaagcgattct
cctgcctcagcctcctgagtagctgggattacaggcacgcaccaccatgtctggctaatttttgtgttttttagtagagat
agggtttcgccgtgttggctaggctggtctggaattcctgacctcaggtgatccaccgcctcgccctcccaaagtgtg
ggattacaggcgtgagccactacgcccagccctgtttcagtccttaactcgcttcttgtcataagaaaaagcatgtgag
tttgaggggagaaggtttggaccacactgtgcccattgcttcccacagcagtaaagtcacaggacagactgtggcaggc
ctggcttccaatcttggctctgcaacaaatgagctggttagcctttgacaggcctgggctgtttcttccacctctgaatta
gggaggctggaccagaaaactcctgtggatcttgtcaactctggtattcttagagactctgtttgggaaggagtcctgag
ccatttttttttcttgagaatttcaggaagaggagtgcttatgatagctctctgctgcttttatcagcaaccaaattgc
aggatgaggacaagcaattctaaatgagtacaggaactaaaagaaggcttggttaccactcttgaaaataatagctagtc
caggtgcggggtggctcacacctgtaatctcagtattttgggatgccgaggtggactgatcacctaaggtcaggagttcg
aaaccagcttggccaatgtggcgaaccctgtctctactaaaaattcaaaaattagccaggcatggtggcacatgcctgt
aatcccagttacttgggaggtgaagcaggagaattgcttgaacctgggaggtggaggtcgaggaggccaaaattgcgc
cactgtactccagcctgagcaacacagcaaaactccatataaaaaataaaatgaataaaataacagctaattctagtc
cagtataactccagtgaacagaagatttattaggcatagtgaatgatggtgcttctctaaaaatctcttgactacaaagaa
tctcatttcaatgtttattgttttagatgttcagaataaattcttgggaaagaccttggcttgggtgaagtgaattaccag
tgccgagggcagggtgaaccaagtctcagtgctggttgactgagggcagtgctggtgacctgtagtcagggttccggtca
cactgtggacatggtcactgttgccttgatttgttttctgtttcaattcttgtctataaagaccgtagcttgggttt
catgtgatgacagAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCCGATTATCTGGTGA
AGACGTATGTGCAGATCATAGCCAAAAGgtgacttttactaaacttggccctgccttattattactaattagaggaat
taaagacctacaaataacagactgaaacagtgggggaaatgccagattatggcctgattctgtctatttggaggttagga
tattatcccaaactagaaaagatgacgagagggactgtgaacattcagttgtcagcttcaaggctgaggcagcctggtct
agaatgaaaatagaaatggattcaacgtcaaattttgccac

Fig. 12 (SHEET 23 OF 32)



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SEQ ID NO: 25
Genomic contig containing ABC1 exon 32: _

gcatgctggagtgatagtgaccatgagtttctaagaaagaagcataatttctccatagtcatccacaattgaaatatta
ttgttaattgaaaaagcttctagggcaggcacggtggctcatgcctgtaatcccagcactttaggagccaaggcgggtgg
atcacttgaggtcaggagtttgagaccagcctggccaacatggggaaaccctgtctctactaaaaatacaaaataagctg
ggcgtgggtggtgctgcctgtaatcccagctacttgggaggctgaggcaggagaactgcttgaatctgggaggcggaggt
tgcagtgagctgagttcatgccattgcattccagcctgggcaacaagagcgaaaccatctccaaaagaaaaaaaaaga
aagaaaaagcttctagtttggttacatcttgggtctataaggtgggtttgtaaattggtttaaccaaggcctggttctcat
ataagtaatagggtatattatgatggagagaaggctggaagaggcctgaacacaggcttcttttctctagcacaaccctac
aaggccagctgattctagggttatcttctgtccgttccttatatcctcaggtggatatttactccttttgcattcattagga
ataggctcagtgctttctttgaactgattttttgtttctttgtctctgcagCTTAAAGAACAAGATCTGGGTGAATGAGT
TTAGgtaagttgctgtctttctggcacgttttagctcagggggaggatggtgtttaggtgtgcttggttgaagaaagcc
ttggggattgtttgtcactcacacacttgtgggtgccatctcactgtgagga

Fig. 12 (SHEET 24 OF 32)



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SEQ ID NO: 26

Genomic contig containing ABC1 exon 33 to 36:

gctttatagagtttctgcctagagcatcatggctcagtgcccagcagccccctccagaggcctctgaatatttgatatact
gatttccttgaggagaatcagaaatctcctgcaggtgtctagggatttcaagtaagtagtggtgtgaggggaatacctac
ttgtactttcccccaaaccagattcccagggcttcttaaggactcaaggacaatttctagggcatttagcacgggactaa
aaaggtccttagaggaaataagaagcgccaaaaccatctctttgactgtatttcaaccatttgccttctgggttttga
aggaacaggtgggactggggacagaagagttcttgaagccagtttgcctcatggaaaatgagataggtgatgtggcta
cgtcagggggcccgaaggctccttggtactgatttccgtcttttctctctgccttttccccaaagggccaggacccttggg
tctctgggcagagcagcagggccctataatagccctcatgctagaaaggagccggagcctgtgtataaggccagcgc
agcctactctggacagtgcaggggtcccactctcccaactccccatctgcttgccctccagaccacattcacacacgagc
cactgggttgaggagcatctgtgagatgaaacaccattcttctcctcaatgtctcagctatctaactgtgtgtgtaatca
ggccaggtcctcctgtgtgggcagaaaccatgggagtttaagagattgccaacatttatttagaggaagctgacgtgtaact
tctgaggcaaaatttagccctccttgaacaggaatttgactcagtgaaacctgtacacactcgactgagctgtgtgtgt
gatgatactgtgcacccactgtctgggttttaatgtcaggtgttcttttagGTATGGCGGCTTTTCCCTGGGTGTCAG
TAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGg
taaaatctctatcgtaagatgtatcagaaaaatgggcatgtagctgtctgggatataaggagtagttggcaggttaaacgga
tcacctggcagctcattgttctgaatatgttggcatcacagaccgtcttggcatttagcgatttgagccagacaaaact
gaattacttagttgtacgtttaaaagtgtaggtcaaaaacaaatccagaggccaggagctgtggctcatgcctgtaatcc
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ggagaattgcttgaacctgttaggaagaggttgtagttagccaagatcgaccgttgcactccagcctgggcaacaagag
caaaactccatctcaaaaaacaaattaaatccagagatttaaaagctctcagaggctgggcgcggtggcttacacctgtt
atcccagcattttgggatgccgagggcgggcaagcacaaggtcaggagtttgagaccagcctggccaacatagtgaacc
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gcaagactccatctcaaaaaagctctcagaacaaccaggtttacaaatttggtcagttggtaataaactgggtttcaa
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taggacctgataagtactcacttctctgtgtctcaggtttcccattttaggtgagaattaaggggctctgataa
aacagaccctaggattgtggacagcagtgatagtcctagagtccacaagtctgcttttgagtgatgggccccatgtatctg
gcacatctgcaggcagagcgtggttctggctcttcagatgatgccggtggagcactttgaggagtcctcaccaccagctg
ataaccagacattaaaatcttggggctttgcatcccaggatttctctgtgattccttctagacttgtggcatcatggcag
catcactgctgtagatttctagtcacttgggttctcaggagccgtttatttaattggcttcacatttaatttcagtgaacaa
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gtcacaaactgaggcaggtttctgttgtttacagGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGAC
AGGACTGGACACCAGAAATAATGTCAAGgtaaaccgtgtcttctgttagtagctttttgatgaacaataatccttatg
tttcttgagtagtcttcaactcatggtaaagtggcaggggcatccacaacagaaaagagcaaaactattaactttaccag
tgaggcagtagcgtgtagtgtagtgattcagagaatttgctttgccaccagacataaccaggtaaccttgactaagttact
taacctatctaaacctcagttcctcatctgtgaaatggagacagtaatcatagctatttccaaactgttgtagaattc
aatgagttaaaggtataaggtcctcaccacagcgcctgcccacatagtcagtgatcactatgtcctgaacactgtaatta
cttcgccatattctctgatcatagtggtttgccttggtatgtgactagaatttctttctgaggtttatgggcatgggtgg
tgggtatgcacctgctgcaggagcccgtttgggggcatccttgtagcttggtatgttttcttccagGTGTGGTTCAA
TAACAAGGGCTGGCATGCAATCAGCTCTTTCTGAATGTTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAG
AGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTg
taagtgtggctgtgtctgtatagatggagtggggcaaggagaggggttatggagaaggggagaaaaatgtgaatctcatt
gtaggggaacagctgcagagaccgttatattatgataaatctggattgatccaggctctgggcagaagtataagtttac
gaattggctgggttgggcttcttgaactgcagaagagaaaaatgacactgatatgtaaaaatcgtaacatttagtgtaattca

Fig. 12 (SHEET 25 OF 32)



tataaagtgagttcaaaaattgttaattaaattataaatttaattataaagtgtttaatcagtttgatttgtttaaaaacca
ctgttttaaaatttggtggaatatgtttttattagcttgatctttaattcctaaattaagctgtgtgtgtgtgtgtgtgt
gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgaagtttaagccaggatgagctagtttaagtatgcagcctttggagtc
atacagatctgggtttgaatctggtctctaaactttatagatgtatgatattaaatgaggcagttcatgtaaattgcca
gcccagcactcagcacagagttgataatttcacacacattagataacctttcctgtatgtggagcatggcagttcctgtttc
tgctttactcctacaggataactaatataggacactaggatctttataccaagaccccatgtaatgggcttatgagaccat
tcttcttataaaaaatctgacagaatttttgatgtgttagatcaataggctgcatactgttattttcaagttgatttaca
gccagaaatattaattttatttgagtagttacagagtaataatttctgctctcatttagttttcaagccccactagtccttt
gtgtgtgaaaatttacaacttactgctcttacaaggctcatgaacagtggaacaaagtgaatgccattaaccactctgact
tccttcattagttttattgtgacagtggaactcttttgacctcagtaataaccagtttggcatttacattgtcatattttta
gacttaaaaaatgatcatcttaacctgaataaaatgtgtctggtgaacagatgtttttccttggtgtgcctcagatata
tctgtgtgtgtgtacgtgtgtgtttgtctgtgtgtccatgtcctcactgattgagccctaactgcatacaagacccctca
gattttcacacgctttttctctccagGATGACCACATCAGTGGATGTCTTGTGTCCATCTGTGTTCATCTTTGCAATGTC
CTTCGTCCAGCCAGCTTTGTCTGATTCCTGATCCAGGAGCGGGTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAG
TGAAGCCTGTCTACTTGGCTCTCTAATTTTGTCTGGGATATGgtaaggacacagggcctgctgtatctttctgatgtct
gtcagggccatggattgatatggataagaaagaaagagctctggctatcatcaggaaatgttccagctactctaaagatg
tatgaaaaagaaatagccagagggcaggtgatcatttcatgacaccaaacacagcattgggtaccagagttcatgtcaca
ccagaggggaaaattctgtacacaaatgatgaaaattaataccactaccacttaagttcctatgtgacaactttcccaagaa
tcagagagatacaagtcaaaaactccaagtcaatgcctctaacttctctgatgggttttaacctccagagtcagaatgttc
tttgcccttactaggaaagccatctgtcatttagaaaactctgtacattttatcagcagcttatccatccattgcaaatat
tgtttttgtgccasccacaatatattgcttctatttggaaccaatatgggggatttgaaggaattctgaagttctaattat
atttcaactctactttacaatatctccctgaaatatatctccctgtaacttctattaattataagctacacagagcaaat
ctaattcttctcccaccgaacaagtccctggatatttaaaaaataactctcactctcatttaacctgagtattaccag
ataagatgatatatgagaatacaccttgtaacctccgaagcactgtacaaatgtgagcaatgatgggtggagatgatgatg
agatctttgctgtttataccaagcccccttagactgtgtcactcttctgatccggttgctccttgatggccatgctgtata
ttgtgaatgtcccgttttcaaaagcaaaagccaagaattaaccttggtgttcaggctgtggtctgaatgggttatgggtccag
aggagttgatctttagctcacacttctattactgcagcacaaagattttgcattttggaaggagcaccgtcttactggc
aacttagtggtaaaccaaaccctccatttcacacaaatgattgtgaaattcgggtctccttcattctatacaaattcatt
tgatttttttgaaactaaactttatatttatccatattaaattacatgggttttatttttgttttatcttgattcagtaa
ttactcctttcagtaaacacagactgagtgtgtgtgtgtgacttatgccaggcatagggtgattcagagatgaaaggta
agtcctgaacctatctctgtcttctgggtattatctgtcctcctgcttttagagctcctgaaatttgctagaagca
tgtcttcatctaagttgttgataaacacatcaagtaggattggactgaggcagagccctgtagtctgaagctgcagttct
tctagcggctgacaagccccactataccttccctgctggtgctttgtctgccagctgtgaattctcataattgtcctat
cgtcaagctctttatttctgcattttactgcttgatacactgtcaggacagactttaaaattattctcagtgcgatgaaac
aattctgacattcatgttatgagcagttacctcataaatagattacatg

Fig. 12 (SHEET 26 OF 32)



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SEQ ID NO: 27

Genomic contig containing ABC1 exon 37 to 41:

aaattactctgactgggaatccatcggttcagtaagtttactgagtgtagacaccttggcttgactggttgaaagacagaaa
gggcatgtagtttataaaatcagccaaggggaaaatgcttgtaaaatgtattgtcggttattttgattaatagtttatg
tggcttcattaattcagagttactctccaatatgtttatctgccctttcttgtctgataatggtgaaaacttgtgtgatg
cattgtatatttgatttaggggtgaactggatgtctttgttttcaacttttagTGCAATTACGTTGTCCCTGCCACACTGG
TCATTATCATCTTCATCTGCTTCCAGCAGAACTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTTCTACTTTTG
CTGTATGGGtaagtcacctctgagtgagggagctgcacagtggataaggcatttgggtgcccagtgtcagaaggagggcag
ggactctcagtagacacttatcttttgtgtctcaacagGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGT
TCAAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAATGGCAGCGTGGCCACCTTT
GTGCTGGAGCTGTTACCGACAATgtgagtcagtcagagagaacactcctgctgggatgagcatctctgggagccagagg
acagtggttaattgtgatcttattccacttgtcagtggtattgacactgctgactgccttgtcctgtcttcagagtcctgt
cttccctgagaaggcaaacgacctttctttcttgtgtgccttacattttgtgtggtcaagcctttcagtttcttttgaca
gttttttttacttctttcttttttcaatgttgctcttaccagagtagctcctctgccttccactttacacatgagagct
gggagcgcattcagtcctaaggcttttaccatcacctctcttgggtgtttttattgtcatctctaagatcaatgccttta
gccttgatcataaccttgaactctaattctcaaatctcacttgcctagtggttgcctcatttagatagtatatagatac
cccaacctggatagtcctagttttctttcccttggaaacttaagcttttcttgcctcctgtcacactcagtggtcac
taccatccactcggttggccaagctgggtctttagagttatcctagatgcttgccttgccttgcagatttcccacattca
actggttatgttgtagtcttccaggtatggacctctaaaataaggcttccctctccattccggttgcattgcctttgt
ccaaacacagcacacaaggccttttacagttgcacaactcttccgtgcataaccaccacacccctttccagctgtaagc
ttcagatgagttgcctccaaccacatgctcctgtaggcctggcttgaaatgcccttcttctgtcacagggtctggtagt
atatcccttgccttcaagatttagctaaaatgtgaagctttccttacctgctgggaggtgttctctcttttctctgtgc
tctcagagtccttagtccatgcctccagtagaacgtacatccacttacatggtaatttccgtgtttacatacttttccctac
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gttggtagatatttggccactgttgccttgtgggatcataagttctgatgtatttgagaagaatttctaaaattctgaca
aaatcctgaaactcaaatattgaccagacatgagcaatttgccttttcaaatgctaagggtatttttaattggatttgcctt
aattaaatctagcctgtttctaaagctttattcattatttctccatactcagagcatttctccagattttctaaagaatag
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agaatcaaattttttcttccactcccatatttcagaacttgatacatttttaggataaaccatgaatgacacccgtttctt
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CGTGTTCCTTGATCTTCCACATTTTGCCTGGGACGAGGGCTCATCGACATGGTGAAAAACCAGGCAATGGCTGATGCC
TGGAAGGTTTGgtgagtgagcagtggtgtgaggtgctttaaaggagatggcactctgcataggccttggtagcctga
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acagctgggttggcatgggttttgtgacacaaccatttgtctgtgtctctgatagcattgagaaaagtgaaggggcag
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aagtcaaaccataactttgagaattaggtgatcagggaaatcagaaggaaagatgcaaactttgggtcttttaggcgaatc
atgtgcctgcagatgaggtcatttattatcttttacacagctctataaaattataatgtattacatctttttctaccttta
gaatgggttaaaaatatttctccggtagccatagattattattcatccattagataatagtcgaatgggcatgttat
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aactagatttaattgaatctagtggttttaattgattcactaggatatatgctactgaaaggggaatctgcttaaagtgt
ttctgatatttatttactaaaacttagaatttataaaaaactgactgtgaaaattacttgggtcggttgccttttt
aaaaggatttttggcatgtctcattaaaaaaaagaaatactagatatcttcagtggaagttacaaatcgaatacacattggc
tctgaaattctgattgatactgggtcataaaaagttttcccaaatcagacttggaaagtgatcactctcttgttactctt
ttttccttgtcatgggtgatagccatttgtgtttatttgaagatcggtgaattttaaaggacataggcccaatttgagg
aaggggccatgggtttttagtccctccattctgaccggatctctgcattgtgtctactagGGGAGAATCGCTTTGTGTACCC
ATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGGGTGGTGTCTTCTCATTACTGTTCTGA

Fig. 12 (SHEET 27 OF)



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TCCAGTACAGATTCTTCATCAGGCCAGgtgagctttttcttagaaccgctggagcacctgggtgaggggtcacagaggag
gcgcacagggaaacactcaccaatgggggttgacattgaactgaactcaaaatatgtgataaaactgattttcctgatgtg
ggcatcccgcagccccctccctgccatcctggagactgtggcaagtaggtttataatactacgttagagactgaatct
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AATGATGAAGATGAAGATGTGAGGCGGGAAAGACAGAGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAA
GGAGTTGACGAAGgtgagagagtacaggttacaatagctcatcttcagtttttttcagctttatgtgctgtaaccagca
gtttgctgacttgcttaataaaaaggcatgtgttcccaaaatgtacatctataccaagggtctgtcaattttattttaaa
aacaccatggagacttcttaagaattcttactgagaattcttttgtgatatgaattccattctcgaatactttgggtt
tatatgcttacatttatgtgttagttattaaaacataactaattgttatatctagtcaaactgagtagagagataatggt
gatt

Fig. 12 (SHEET 28 OF 32)



SEQ ID NO: 28

Genomic contig containing ABC1 exon 42 to 45:

ttttaaaatacctgcaatacatatatatgttgaatagatgaaaaattatgtagatgataatgaatgatacggttctaaaa
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gctcttggcacatcaaataatgcctatggcttagggtatttgacaagtcttatgttgagtgatgtggtttatagtcctg
ccttccacagttgcttgggagagctgtgagtcactgaggcttatgaatgtttacattttgtttgttgagATATATAGAA
GGAAGCGGAAGCCTGCTGTTGACAGGATTTCGCTGGGCATTCTCTCGGTGAGGtaagacactttgtctatattgcgtt
tgtccctattagttcagactatctctacccaatcaagcaacgatgctcgtaagaggtaaaagtggattttaaggcttc
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cggactcacgaggtcaggagattgagaccatcctggccaacatggtgaaaccccatctctactataaaatacaaaaattag
ctgggcatagtagtgactcctgtagtcacagctactcgggaggtgagggcaggagaattgcttgaacctaggaggggga
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cacatctaaaacatgctttttgtatccatttgggatggtgatgacattcaaatagttttttaaaaatagattttctcctt
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tgaaatacatattttaaatatctatacagatgtgtttaaaccagaagaaatatttgattcttctctgatatttaagaattgaa
ggtttgaggtagttacgtgttagggcatttatattcatgttttttagagtttgcctatacaacttaattctttccttttca
gTGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACAGGAGATACCACTGTTACCA
GAGGAGATGCTTTCTTAACAAAAATAGgtgagaaaaagaagtggcttgatttttgctgcaaagactttgtttttaattta
tttaagaaataggttgattttttgattacagtggtatttttagagttcataaaaatggtgaaatatagtaaagggttaa
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taaattgtccatacaattgagatcactgtatgtagaatttaaaattagttttttattgttaattgagtgattatgaata
tttcccagtggttacatttccctaagatgtggaattttacattgctacataaaatccccctatgtacatgtacctataat
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gagccactgcgcccggcttctctggacttattatgtggagagatagtagaaggcagtggtttcagagttttttgacct
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tggttggtaaagaatgtgcagtggttgcatgacctcagaattctgaaatgggactgcacctgcagactgaagtgttcag

Fig. 12 (SHEET 29 OF 32)



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agagccagggaggtgcaaggactggggagggtagaggcaggaaccctgcctgccaggaagagctagcatcctgggggcag
aaaggctgtgctttcaagtagcagcagatgtattggtatctttgtaatggagaagcatactttacaggaacattaggcca
gattgtctaaccagagtatctctacctgcttaaaatctaagtagttttcttgcctttgcagTATCTTATCAAACATCCA
TGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTGTTGACTGGGAGAGAACACGTGGAGT
TCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAAGTTGGCAAGgtactgtgggcacctgaaagccagcctgtctcctt
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Fig. 12 (SHEET 30 OF 32)



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SEQ ID NO: 29

Genomic contig containing ABC1 exon 46 to 49:

ngccnngttnaaaangaaaatttnnnnnnaaattnaannttanngngnnntttccccagaaaaacnaaaangatttccn
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tccccaaaaacctattattgagaatttaattacataaaaaagttactcagaatatttgagtttctctgcatcaataagacat
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CCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACATCTCATAGgtccgtagtaaagtcttgggttctctactgt
gggatgttttaactttccaagtagaatatgcatcattttgtaaaaattagaaaatacagaaaagcaagagtaaaacaa
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TGCCAAGGACCAAAGTGATGATGACCATTAAAAGACCTCTCATTACACAAAAACCAGACAGTAGTGGACGTTGCAGTTC
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taattcatcaagtaatcatggccagcgattattgatcaaaatcaaaaggtaatgcacatcctcattcactaagccatgcc

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atgccaggagactgggtttcccggtgacacatccattgctggcaatgagtggtgccagagttattagtgccaagttttca
gaaagtttgaagcaccatgggtgtgtcatgctcacttttgtgaaagctgctctgctcagagtctatcaacattgaatatca
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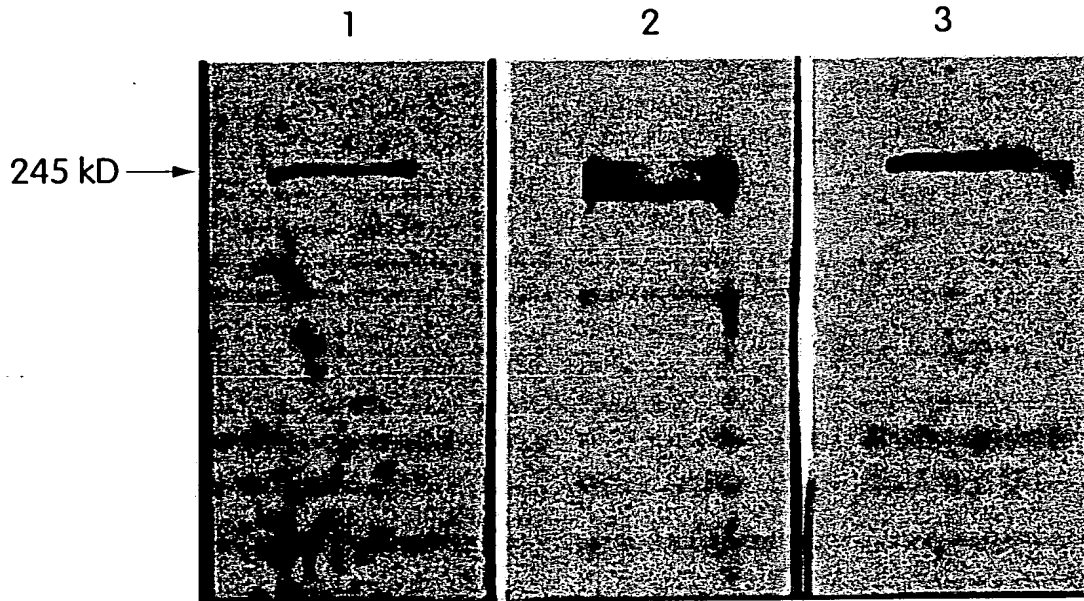
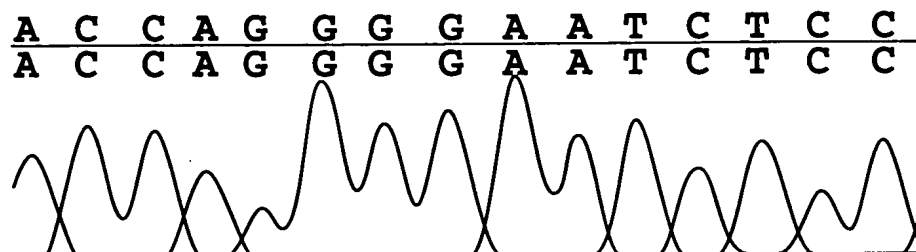


Fig. 13



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Control



WHAM

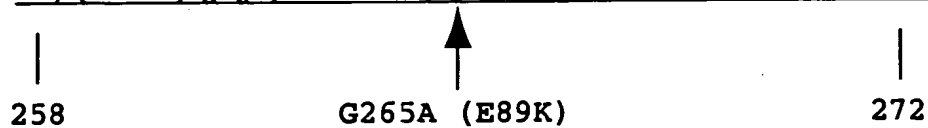
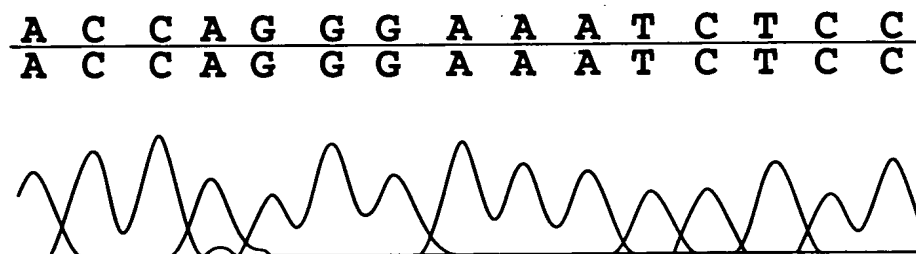


Fig. 14

Serial No.: 09/526,193
Applicant: Hayden et al
Filed: 15 March 2000
Attorney Docket: 760050-19

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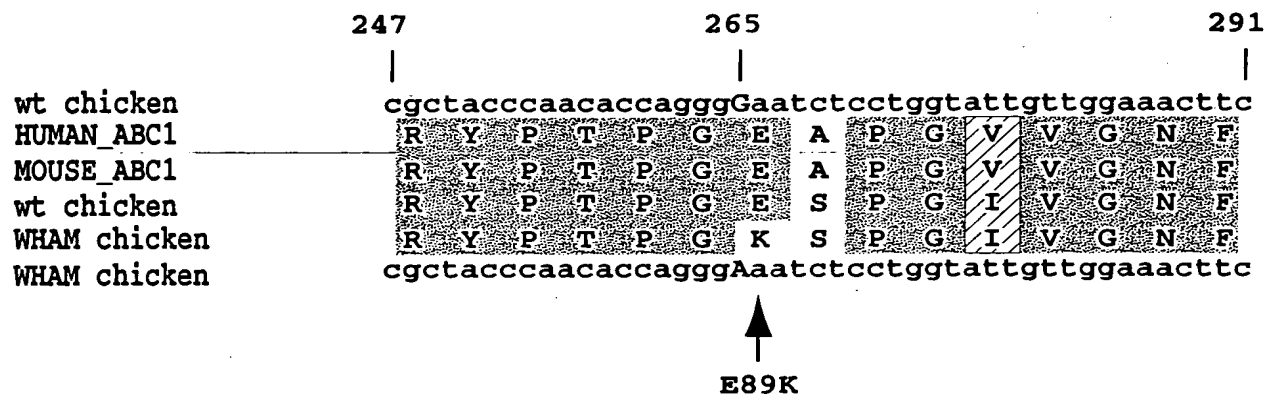


Fig. 15

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No. Name	Location in SEQ ID No. 14	Sequence	Sequence Strand Length
1 PPPE	58-69	AGGTAAAGTCA	12 Complement
2 PPPE	1997-2009	AGAGTAGAGGCA	13 Lead
3 PPPE	2150-2161	ATGTCAAGTTCA	12 Lead
4 PPPE	2156-2169	AGTTCAAAAGGCA	14 Lead
5 PPPE	4126-1139	AGGCCAGAGGGCC	14 Complement
6 PPPE	5075-5087	AGGCAGAGTGA	13 Lead
7 PPPE	6604-6615	ATGCCAAGGTCA	12 Complement
8 PPPE	6731-6743	GGGCCAAGGGTA	13 Complement
9 PPPE	7220-7233	AGGTAATGAGGACA	14 Complement
10 PPPE	7554-7568	GGATCAGAGGTCA	15 Complement
1 SRE	159-166	CAGCCCAT	8 Lead
2 SRE	1133-1140	CAGCTCAC	8 Complement
3 SRE	1145-1152	CACACCCAC	8 Lead
4 SRE	1809-1816	CAGCCCTC	8 Complement
5 SRE	1894-1901	CAGCCCAT	8 Lead
6 SRE	2563-2570	CAACCCAC	8 Lead
7 SRE	3303-3310	CAGCTCAC	8 Lead
8 SRE	3470-3477	CCGCCAC	8 Lead
9 SRE	4784-4791	CTCCCCAC	8 Lead
10 SRE	4802-4809	CAGCCTAC	8 Complement
11 SRE	4970-4977	CACCTCAC	8 Complement
12 SRE	6487-6494	CAGCCTAC	8 Complement
13 SRE	6565-6572	CACCCAAC	8 Complement
14 SRE	6727-6734	CACCCCTCA	8 Lead
15 SRE	7041-7048	CACCCAAC	8 Lead
16 SRE	8059-8066	CAGCCCTC	8 Complement
1 ROR (retinoic acid receptor related)	166-172	AGGTCA	7 Complement
2 ROR (retinoic acid receptor related)	166-173	AAGGTCA	8 Complement
3 ROR (retinoic acid receptor related)	263-370	ATGGGTCA	8 Lead
4 ROR (retinoic acid receptor related)	264-370	TGGGTCA	7 Lead
5 ROR (retinoic acid receptor related)	2218-2225	TAGGTCA	8 Lead
6 ROR (retinoic acid receptor related)	2219-2225	AGGTCA	8 Lead
7 ROR (retinoic acid receptor related)	3643-2649	TGGGTCA	7 Lead
8 ROR (retinoic acid receptor related)	6604-6610	AAGGTCA	7 Complement
1 SREBP-1 or "E box"	473-479	ACACCTG	7 Complement
2 SREBP-1 or "E box"	536-541	ACACATG	7 Lead
3 SREBP-1 or "E box"	537-543	TCATGTG	7 Complement
4 SREBP-1 or "E box"	655-661	TCATGTG	7 Complement
5 SREBP-1 or "E box"	925-931	ACACTTG	7 Lead
6 SREBP-1 or "E box"	967-973	TCACTTG	7 Lead
7 SREBP-1 or "E box"	968-974	TCAAGTG	7 Complement
8 SREBP-1 or "E box"	1053-1069	ACAGGTG	7 Complement
9 SREBP-1 or "E box"	1104-1110	TCACCTG	7 Lead
10 SREBP-1 or "E box"	1105-1111	TCAAGTG	7 Complement
11 SREBP-1 or "E box"	1561-1567	TCACTTG	7 Lead

Fig. 16 (SHEET 1 OF 2)



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12	SREBP-1	or	"E box"	1670-1676	TCAAATG	7	Lead
13	SREBP-1	or	"E box"	1748-1754	ACACTG	7	Lead
14	SREBP-1	or	"E box"	1749-1755	ACAAATG	7	Complement
15	SREBP-1	or	"E box"	1852-1858	TCATGTG	7	Lead
16	SREBP-1	or	"E box"	1853-1859	ACATGTG	7	Complement
17	SREBP-1	or	"E box"	1899-1905	ACAAATG	7	Complement
18	SREBP-1	or	"E box"	2199-2205	ACACGTG	7	Lead
19	SREBP-1	or	"E box"	2393-2399	ACAGGTG	7	Complement
20	SREBP-1	or	"E box"	2669-27005	ACACCTG	7	Lead
21	SREBP-1	or	"E box"	2677-2683	TCACATG	7	Complement
22	SREBP-1	or	"E box"	2740-2746	ACAACTG	7	Complement
23	SREBP-1	or	"E box"	2969-2975	ACAAATG	7	Lead
24	SREBP-1	or	"E box"	2979-2985	ACACATG	7	Lead
25	SREBP-1	or	"E box"	2981-2987	ACATGTG	7	Lead
26	SREBP-1	or	"E box"	2980-2986	ACATGTG	7	Complement
27	SREBP-1	or	"E box"	2982-2988	ACACATG	7	Complement
28	SREBP-1	or	"E box"	3461-3467	TCAGGTG	7	Lead
29	SREBP-1	or	"E box"	3462-2468	TCACCTG	7	Complement
30	SREBP-1	or	"E box"	3547-3553	TCAACTG	7	Complement
31	SREBP-1	or	"E box"	3752-3758	ACACATG	7	Lead
32	SREBP-1	or	"E box"	4226-4232	TCACCTG	7	Lead
33	SREBP-1	or	"E box"	4582-4588	ACACGTG	7	Complement
34	SREBP-1	or	"E box"	4588-4594	TCAGTTG	7	Lead
35	SREBP-1	or	"E box"	4861-4867	TCAGGTG	7	Lead
36	SREBP-1	or	"E box"	4951-4957	ACAAATG	7	Lead
37	SREBP-1	or	"E box"	5096-5102	TCAAATG	7	Complement
38	SREBP-1	or	"E box"	5912-5918	ACAGTTG	7	Lead
39	SREBP-1	or	"E box"	5913-5919	TCAACTG	7	Complement
40	SREBP-1	or	"E box"	6245-6251	ACACATG	7	Complement
41	SREBP-1	or	"E box"	6288-6294	ACAACTG	7	Complement
42	SREBP-1	or	"E box"	6623-6629	TCATTTG	7	Lead
43	SREBP-1	or	"E box"	6836-6842	TCACCTG	7	Lead
44	SREBP-1	or	"E box"	6837-6843	ACAGGTG	7	Complement
45	SREBP-1	or	"E box"	7032-7038	ACAGGTG	7	Complement
46	SREBP-1	or	"E box"	7069-7075	TCAGGTG	7	Lead
47	SREBP-1	or	"E box"	7101-7107	ACATATG	7	Complement
48	SREBP-1	or	"E box"	7138-7144	ACAGTTG	7	Lead
49	SREBP-1	or	"E box"	7139-7145	TCAACTG	7	Complement
50	SREBP-1	or	"E box"	7240-7246	ACACCTG	7	Complement
51	SREBP-1	or	"E box"	7467-7473	ACAGGTG	7	Lead
52	SREBP-1	or	"E box"	7640-7646	TCATTTG	7	Lead
53	SREBP-1	or	"E box"	7641-7647	TCAAATG	7	Complement
54	SREBP-1	or	"E box"	7653-7659	TCAGTTG	7	Lead
55	SREBP-1	or	"E box"	7654-7660	ACAACTG	7	Complement
56	SREBP-1	or	"E box"	7735-7741	ACAAATG	7	Lead
57	SREBP-1	or	"E box"	7838-7844	TCAGGTG	7	Complement
58	SREBP-1	or	"E box"	7880-7886	TCATCTG	7	Complement
59	SREBP-1	or	"E box"	8051-8057	TCAGCTG	7	Lead
60	SREBP-1	or	"E box"	8052-8058	TCAGCTG	7	Complement

Fig. 16 (SHEET 2 OF 2)